GenCore version 5.1.6


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Run on: April 7, 2004, 16:59:33 ; Search time 52.9316 Seconds
(without alignments)
1362.959 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| | 3 | 694 | 100.0 | 1849 | 4 | US-09-345-790-1 | Sequence 1, Appli |
| | 4 | 84.5 | 12.2 | 3666 | 4 | US-09-107-532A-305 | Sequence 305, App |
| | 5 | 83.5 | 12.0 | 1008 | 4 | US-09-354-138-130 | Sequence 130, App |
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| c | 14 | 74 | 10.7 | 2925 | 4 | US-09-540-236-384 | Sequence 384, App |
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| | 20 | 71.5 | 10.3 | 3650 | 4 | US-09-620-312D-30 | Sequence 30, Appl |
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| | 26 | 71 | 10.2 | 699 | 2 | US-08-230-428B-1 | Sequence 1, Appli |
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ALIGNMENTS

RESULT 1
US-08-912-227-1
; Sequence 1, Application US/08912227
; Patent No. 5998171
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,227
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,058
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-08-912-227-1

Alignment Scores:
Pred. No.:                3.1e-91        Length:          1849
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

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RESULT 2
US-09-513-584-1
; Sequence 1, Application US/09513584
; Patent No. 6406867
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  Human Endokine Alpha and Methods
;    TITLE OF INVENTION:  of Use
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX,
;      ADDRESSEE:  P.L.L.C
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/513,584
;      FILING DATE:  25-FEB-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/024,058
;      FILING DATE:  16-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/912,227
;      FILING DATE:  15-AUG-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/122,099
;      FILING DATE:  26-FEB-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/136,788
;      FILING DATE:  28-MAY-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/345,790
;      FILING DATE:  01-JUL-1999
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0470005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-09-513-584-1

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Best Local Similarity:    100.00%        Mismatches:      0
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; Sequence 1, Application US/09345790
; Patent No. 6521742
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  Human Endokine Alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/345,790
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/912,227
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0470001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-09-345-790-1

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Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
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Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 4
US-09-107-532A-305
; Sequence 305, Application US/09107532A
; Patent No. 6583275
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 305:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3666 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...3666
;       SEQUENCE DESCRIPTION: SEQ ID NO: 305:
US-09-107-532A-305

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Pred. No.:                0.142          Length:          3666
Score:                    84.50          Matches:         19
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RESULT 5
US-09-354-138-130
; Sequence 130, Application US/09354138
; Patent No. 6309647
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Gettig, Russell
;    TITLE OF INVENTION:  POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
;    TITLE OF INVENTION:  RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
;    TITLE OF INVENTION:  RECOMBINANTS
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue, 25th Floor
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/354,138
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,379
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/416,646
;      FILING DATE:  05-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/224,657
;      FILING DATE:  16-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,962
;      FILING DATE:  08-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/776,867
;      FILING DATE:  23-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/621,614
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,283
;      FILING DATE:  31-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/713,967
;      FILING DATE:  11-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07,666,056
;      FILING DATE:  07-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2860
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1008 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-354-138-130

Alignment Scores:
Pred. No.:              0.026           Length:        1008
Score:                  83.50           Matches:       31
Percent Similarity:     46.30%          Conservative:  19
Best Local Similarity:  28.70%          Mismatches:    34
Query Match:            12.03%          Indels:        24
DB:                     4               Gaps:          6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-354-138-130 (1-1008)

Qy          2 LeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLys 21
              ||||||||||          :::   |||:::  :::   |||   |||
Db        200 CTCCAATTGGAAGAACATTTGGATCGCTGCCTTTAGGAGTTGGGCGTACTACAGCCAGAC 259

Qy         22 TrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrp--------- 38
              :::          :::||||||||||                 |||
Db        260 CTGAGGAGTTATTGAAAGAAGCCACCCTGT-----------------TGGATATTATGG 301

Qy         39 ------LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaPro 56
                    :::|||::::::   :::|||      |||   |||          :::   |||
Db        302 TAAGGCGAACTGCAGGTGTCAAGGAACAACTGGTATTTTATA---------ATAACACCC 352

Qy         57 Asn-AlaAsnTyrAsnAspVal------AlaProPheGluValArgLeuTyrLysAsnLy 74
              ::: |||:::   |||   |||          |||:::|||   :::     :::   ||
Db        353 CATTGCACATCTTAACTCCGTGGAAAAAGGTCCTTACGAGTGGAAGTGTGTTCAGTGCAA 412

Qy         74 sAspMetIle--------------GlnThrLeuThrAsnLysSerLysIleGlnAsnVa 89
              |     :::                  |||:::   :::   :::||||||||||
Db        413 ATCAAGTCTGTAACACAGTCAATCTAATACCATTAGACATAGCACAAAGATTCAG----- 467

Qy         89 lGlyGlyThrTyrGluLeuHis 96
               ||||||   ||||||   |||
Db        468 -GGTGGTATATATGAGCATCAC 488

RESULT 6
US-08-496-944-1
; Sequence 1, Application US/08496944
; Patent No. 6040496
;  GENERAL INFORMATION:
;    APPLICANT:  Law, Marcus D
;    APPLICANT:  Dietz, Jon M
;    TITLE OF INVENTION:  Use of Translationally altered RNA to
;    TITLE OF INVENTION:  Confer Resistance to Maize Dwarf Mosaic Virus and Other
;    TITLE OF INVENTION:  Monocotyledonous Plant Viruses
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  CIBA-Geigy Corporation
;       STREET:  7 Skyline Drive
;       CITY:  Hawthorne
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10532
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/496,944
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Elmer, James Scott
;       REGISTRATION NUMBER:  36,129
;       REFERENCE/DOCKET NUMBER:  CGC 1814
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8543 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  RNA (genomic)
;     HYPOTHETICAL:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  3..8291
;       OTHER INFORMATION:  /product= "polyprotein encoded by
;       OTHER INFORMATION:  MDMV-B genome"
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  8292..8530
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  3..1133
;       OTHER INFORMATION:  /product= "3-prime sequence for
;       OTHER INFORMATION:  HC-Pro"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  1134..2375
;       OTHER INFORMATION:  /product= "P3 proteinase"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  2376..4292
;       OTHER INFORMATION:  /product= "cylindrical inclusion
;       OTHER INFORMATION:  protein"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  4293..4451
;       OTHER INFORMATION:  /product= "K2 (6kD protein)"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  4452..5744
;       OTHER INFORMATION:  /product= "NIa proteinase"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  5745..7307
;       OTHER INFORMATION:  /product= "NIb replicase"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  7308..8291
;       OTHER INFORMATION:  /product= "coat protein"
US-08-496-944-1

Alignment Scores:
Pred. No.:              6.75          Length:          8543
Score:                  77.00         Matches:         31
Percent Similarity:     41.13%        Conservative:    20
Best Local Similarity:  25.00%        Mismatches:      53
Query Match:            11.10%        Indels:          20

DB:                     3             Gaps:            5

US-09-195-368-1_COPY_48_177 (1-130) x US-08-496-944-1 (1-8543)

Qy          4 LeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGln 23
              ::::::      ||||||   |||      ||||||      |||||||:::   ||||||
Db         54 AUACAAUUUAUCAAAGAAAGGUGCAAUCCAAAAUUUUCGCAUUUACCAACGCUAUGGCAA 113

Qy         24 MetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeu 43
              :::|||   :::          :::      |||       :::::::::
Db        114 GUCGCGGAAACAAUAGGGCACUAUACUGAUAACCAGUCAAAGCAAAUAAUGGAUGUU--- 170

Qy         44 GlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspVal 63
                  |||      :::          :::|||
Db        171 AGCGAAGCGCUCAUCAAAGUUAAUACUCUGACUCCUGAUGAUGCUAUGAAAGCAAGCGCA 230

Qy         64 AlaProPheGluVal---ArgLeuTyrLysAsnLys----------------AspMet 76
              |||      ||||||   |||   |||||||||:::              |||
Db        231 GCGUUACUUGAAGUGUCGCGAUGGUAUAAGAAUCGUAAGGAGUCACUCAAAACUGACUCA 290

Qy         77 IleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHis 96
              :::::::::      ||||||                                :::
Db        291 UUGGAAUCUUUUAGAAAUAAA--------------------------------AUAUCA 317

Qy         97 ValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsn---Asn 115
                  ||||||:::               ::::::|||:::   ||||||   |||
Db        318 CCAAAGAGUACAAUAAAUGCAGCUUUAAUGUGCGAUAAUCAAUUGGAUAAAAAUGCAAAU 377

Qy        116 ThrTyrTrpGly 119
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Db        378 UUUGUAUGGGGU 389

RESULT 7
US-08-998-416-717/c
; Sequence 717, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
```

```
;  INFORMATION FOR SEQ ID NO:  717:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1470RP
US-08-998-416-717

Alignment Scores:
Pred. No.:                0.303          Length:         699
Score:                    74.50          Matches:        37
Percent Similarity:       40.60%         Conservative:   17
Best Local Similarity:    27.82%         Mismatches:     60
Query Match:              10.73%         Indels:         19
DB:                       3              Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x US-08-998-416-717 (1-699)

Qy          3 GlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyPro------LeuProSer 20
              :::|||||||||                    ::::::      |||
Db        444 GAGCTTGAGACTGAGCTCGCGCGGATGAAGAGCGAGATGGTACCGCAGCTGTTCATGCAG 385

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              |||     |||  :::      |||     ||||||:::::|||   :::    |||
Db        384 AAGCACGTTATGGGCACGGTGTCCCCC------GTGAACAGACTTTCGCAGTTCCATCTT 331

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
                 |||   :::   |||      :::   ||||||     :::      |||
Db        330 GTGATAGAGAAGCAGGGCCGCACGATCTTCTACGGGCCGACTTCATTTCGAGCGGTCGTC 271

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              :::   |||:::|||          |||   |||   .        :::|||   |||
Db        270 GATTCTGTGAGTCCG---------CGGTTCTACCATTATTTTACTGTAATCCTGACGAAG 220

Qy         81 ThrAsnLys--------------SerLysIleGlnAsnValGlyGlyThrTyrGluLeu 95
                                    |||      |||                  ||||||
Db        219 TTGCGGCATGTGCGTCTGTCTTGGAAGAAAGATAATAACTACTCTGCGATGATGGAGCTA 160

Qy         96 HisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsn 115
                 |||   |||:::      |||   |||||||||:::
Db        159 ---------GATTTGATAGAGACACCTTTCATGAGCGAACATGAA-----------CAG 121

Qy        116 ThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPhe 128
              |||     |||   :::||||||      |||   :::
Db        120 ACACTACTGGGGGGGCTTCTGCTGCGTCTTCCGAGCTAT 82

RESULT 8
5182196-3
;Patent No. 5182196
;     APPLICANT: ALLET, BERNARD;KAWASHIMA, ERIC H.
;     TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
;DESIRED PROTEINS
;     NUMBER OF SEQUENCES: 23
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/372,281
;       FILING DATE: 27-JUN-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 53,398
;       FILING DATE: 18-MAY-1987
;       APPLICATION NUMBER: 785,847
;       FILING DATE: 09-OCT-1985
;SEQ ID NO:3:
;       LENGTH: 935
5182196-3

Alignment Scores:
Pred. No.:                0.568          Length:         935
Score:                    74.00          Matches:        37
Percent Similarity:       39.01%         Conservative:   18
Best Local Similarity:    26.24%         Mismatches:     38

Query Match:              10.66%         Indels:         49
DB:                       6              Gaps:           8

US-09-195-368-1_COPY_48_177 (1-130) x 5182196-3 (1-935)

Qy         16 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 35
              ||||||:::||||||   |||   ||||||                        :::|||
Db        510 GGGCCAATGCCCTCC---TGGCCAATGGCGTG--------------------GAGGTG 544

Qy         36 SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnVal--- 54
                |||  :::|||   :::         |||||||||||||||||   ||||||
Db        545 AGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTC 604

Qy         55 --------------AlaProAsnAlaAsnTyr---------AsnAspValAlaProPhe 66
                           |||:::   :::          :::   :::::
Db        605 TTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCAGCCGCATC 664

Qy         67 GluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIle 86
              |||              :::::::::      :::      ||||||
Db        665 GCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATC------AAGAGCCCCTGC 718

Qy         87 GlnAsn----------------------------------------------------ValGly 90
              |||                                                      :::|||
Db        719 CAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTGGGA 778

Qy         91 GlyThrTyrGluLeuHisValGlyAspThrIleAsp------------------------ 102
              |||   ::::::|||      ||||||   :::
Db        779 GGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACTAT 838

Qy        103 LeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeu 122
              |||   |||              ||||||                ||:::||||||||||
Db        839 CTCGACTTTGCCGAGTCTGGGCAGGTC--------------TACTTTGGGATCATTGCC 883

Qy        123 Leu 123
              |||
Db        884 CTG 886

RESULT 9
US-08-697-610-1
; Sequence 1, Application US/08697610
; Patent No. 6172187
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  CD40 Associated Proteins
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/697,610
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/349,357
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1203
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
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```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  137..1766
US-08-697-610-1

Alignment Scores:
Pred. No.:                2.25          Length:         2240
Score:                    74.00         Matches:        28
Percent Similarity:       45.45%        Conservative:   17
Best Local Similarity:    28.28%        Mismatches:     24
Query Match:              10.66%        Indels:         30
DB:                       3             Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x US-08-697-610-1 (1-2240)

Qy          25 AlaSerSerGluProProCysValAsnLysValSerAspTrp------------------ 38
               |||||||||            ||||||   :::   :::|||
Db         818 GCCAGCTCCGCCGTGCAGCACGTCAACCTGCTGAAGGAGTGGAGCAACTCGCTCGAAAAG 877

Qy          39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58
               |||:::   :::|||||||||                              |||      |||
Db         878 AAGGTTTCCTTGTTGCAGAAT-----------------GAAAGTGTAGAAAAAAACAAG 919

Qy          59 Asn------------TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74
               :::            :::|||  :::      ||||||:::   :::  :::   |||
Db         920 AGCATACAAAGTTTGCACAATCAGATATGTAGCTTTGAAATTGAAATTGAGAGACAAAAG 979

Qy          75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94
               :::|||::::::         |||:::||||||||
Db         980 GAAATGCTTCGA------AATAATGAATCCAAAATC---------------------- 1009

Qy          95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113
               ||||||:::         ||||||            |||:::   :::   ||||||
Db        1010 CTTCATTTACAGCGAGTGATAGAC-----------AGCCAAGCAGAGAAACTGAAG 1054

RESULT 10
US-08-349-357-1
; Sequence 1, Application US/08349357
; Patent No. 6265556
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  CD40 Associated Proteins
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/349,357
;      FILING DATE:  02-DEC-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1203
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  137..1766
US-08-349-357-1

Alignment Scores:
Pred. No.:                2.25          Length:         2240
Score:                    74.00         Matches:        28
Percent Similarity:       45.45%        Conservative:   17
Best Local Similarity:    28.28%        Mismatches:     24
Query Match:              10.66%        Indels:         30
DB:                       3             Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x US-08-349-357-1 (1-2240)

Qy          25 AlaSerSerGluProProCysValAsnLysValSerAspTrp------------------ 38
               |||||||||            ||||||   :::   :::|||
Db         818 GCCAGCTCCGCCGTGCAGCACGTCAACCTGCTGAAGGAGTGGAGCAACTCGCTCGAAAAG 877

Qy          39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58
               |||:::   :::|||||||||                              |||      |||
Db         878 AAGGTTTCCTTGTTGCAGAAT-----------------GAAAGTGTAGAAAAAAACAAG 919

Qy          59 Asn------------TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74
               :::            :::|||  :::      ||||||:::   :::  :::   |||
Db         920 AGCATACAAAGTTTGCACAATCAGATATGTAGCTTTGAAATTGAAATTGAGAGACAAAAG 979

Qy          75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94
               :::|||::::::         |||:::||||||||
Db         980 GAAATGCTTCGA------AATAATGAATCCAAAATC---------------------- 1009

Qy          95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113
               ||||||:::         ||||||            |||:::   :::   ||||||
Db        1010 CTTCATTTACAGCGAGTGATAGAC-----------AGCCAAGCAGAGAAACTGAAG 1054

RESULT 11
US-09-645-926A-6
; Sequence 6, Application US/09645926A
; Patent No. 6482411
; GENERAL INFORMATION:
;  APPLICANT:  AHUJA, SEEMA
;  APPLICANT:  BONEWALD, LYNDA
;  TITLE OF INVENTION:  CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
;  FILE REFERENCE:  4003.001000
;  CURRENT APPLICATION NUMBER: US/09/645,926A
;  CURRENT FILING DATE:  2000-08-24
;  PRIOR APPLICATION NUMBER:  60/151,250
;  PRIOR FILING DATE:  1999-08-27
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 6
;  LENGTH: 2339
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-645-926A-6

Alignment Scores:
Pred. No.:                2.41          Length:         2339
Score:                    74.00         Matches:        28
Percent Similarity:       45.45%        Conservative:   17
Best Local Similarity:    28.28%        Mismatches:     24
Query Match:              10.66%        Indels:         30
DB:                       4             Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-645-926A-6 (1-2339)

Qy          25 AlaSerSerGluProProCysValAsnLysValSerAspTrp------------------ 38
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Db        964 GCCAGCTCCGCCGTGCAGCACGTCAACCTGCTGAAGGAGTGGAGCAACTCGCTCGAAAAG 1023

Qy         39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58

Db       1024 AAGGTTTCCTTGTTGCAGAAT----------------GAAAGTGTAGAAAAAAACAAG 1065

Qy         59 Asn----------TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74

Db       1066 AGCATACAAAGTTTGCACAATCAGATATGTAGCTTTGAAATTGAAATTGAGAGACAAAAG 1125

Qy         75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94

Db       1126 GAAATGCTTCGA------AATAATGAATCCAAAATC---------------------- 1155

Qy         95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113

Db       1156 CTTCATTTACAGCGAGTGATAGAC----------AGCCAAGCAGAGAAACTGAAG 1200

RESULT 12
PCT-US95-16980-1
; Sequence 1, Application PC/TUS9516980
;  GENERAL INFORMATION:
;    APPLICANT:  Brigham & Women's Hospital
;    TITLE OF INVENTION:  CONTROLLING TRAF-MEDIATED SIGNALS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16980
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/367,540
;      FILING DATE:  30-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  05311/014WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)542-5070
;      TELEFAX:  (617)542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2359 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  151..1854
PCT-US95-16980-1

Alignment Scores:
Pred. No.:                2.44          Length:          2359
Score:                    74.00         Matches:         28
Percent Similarity:       45.45%        Conservative:    17
Best Local Similarity:    28.28%        Mismatches:      24
Query Match:              10.66%        Indels:          30
DB:                       5             Gaps:            6

US-09-195-368-1_COPY_48_177 (1-130) x PCT-US95-16980-1 (1-2359)

Qy         25 AlaSerSerGluProProCysValAsnLysValSerAspTrp---------------- 38

Db        907 GCCAGCTCCGCCGTGCAGCACGTCAACCTGCTGAAGGAGTGGAGCAACTCGCTCGAAAAG 966

Qy         39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58

Db        967 AAGGTTTCCTTGTTGCAGAAT----------------GAAAGTGTAGAAAAAAACAAG 1008

Qy         59 Asn----------TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74

Db       1009 AGCATACAAAGTTTGCACAATCAGATATGTAGCTTTGAAATTGAAATTGAGAGACAAAAG 1068

Qy         75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94

Db       1069 GAAATGCTTCGA------AATAATGAATCCAAAATC---------------------- 1098

Qy         95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113

Db       1099 CTTCATTTACAGCGAGTGATAGAC----------AGCCAAGCAGAGAAACTGAAG 1143

RESULT 13
US-09-167-109-3
; Sequence 3, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 3
;   LENGTH: 2455
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (218)..(1924)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: U21092
;   DATABASE ENTRY DATE: 1995-03-23
US-09-167-109-3

Alignment Scores:
Pred. No.:                2.6           Length:          2455
Score:                    74.00         Matches:         28
Percent Similarity:       45.45%        Conservative:    17
Best Local Similarity:    28.28%        Mismatches:      24
Query Match:              10.66%        Indels:          30
DB:                       4             Gaps:            6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-167-109-3 (1-2455)

Qy         25 AlaSerSerGluProProCysValAsnLysValSerAspTrp---------------- 38

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Qy         39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58

Db       1034 AAGGTTTCCTTGTTGCAGAAT----------------GAAAGTGTAGAAAAAAACAAG 1075

Qy         59 Asn----------TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74

Db       1076 AGCATACAAAGTTTGCACAATCAGATATGTAGCTTTGAAATTGAAATTGAGAGACAAAAG 1135

Qy         75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94

Db       1136 GAAATGCTTCGA------AATAATGAATCCAAAATC---------------------- 1165

Qy         95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113
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Db       1166 CTTCATTTACAGCGAGTGATCGAC------------AGCCAAGCAGAGAAACTGAAG 1210

RESULT 14
US-09-540-236-384/c
; Sequence 384, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 384
;   LENGTH: 2925
;   TYPE: DNA
;   ORGANISM: M.catarrhalis
US-09-540-236-384

Alignment Scores:
Pred. No.:                3.43          Length:          2925
Score:                    74.00         Matches:         31
Percent Similarity:       39.23%        Conservative:    20
Best Local Similarity:    23.85%        Mismatches:      52
Query Match:              10.66%        Indels:          27
DB:                       4             Gaps:            6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-540-236-384 (1-2925)

Qy         14 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysVal--- 32
Db        451 AAGCTGTCACCATCAAAAAATCGCTGGCAGATTTTTCAACATTCAAACCCGTGCGTTGTA 392

Qy         33 ------AsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIle 50
Db        391 CTGTTTCAGGCAATGAACTCATGGCAGATTGTAATTTAT---------TTTGTACTTGTA 341

Qy         51 TyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeu 70
Db        340 CTTGGGCAG------------------TATCTGGATCAGTGCCATTTTCAA------ATG 305

Qy         71 TyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGly 90
Db        304 TTAAAGTCACAGAGGCAGACCCTGCCGCTGATGAATTTGATGACATGTACATCAGTCCAT 245

Qy         91 -GlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsn---------- 106
Db        244 CAATCCCTTTCATCTGCTGCTCGATGATCTGCGTGACCGAGTTTTCAACCGTCTCAGCAT 185

Qy        107 ---------------SerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIleIl 121
Db        184 CAGCACCTGGGTAGACGGCACGCACCTTTACTTGAGGCGGTGCAATTTTTGG-------- 133

Qy        121 eLeuLeuAlaAsnProGlnPheIleSer 130
Db        132 -GTATTGTTCAATCGGCAAATTATTAAT 106

RESULT 15
US-09-596-002-37/c
; Sequence 37, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
;  APPLICANT:      Lagace, Robert, E.
;  APPLICANT:  Patterson, Chandra
;  APPLICANT:  Berg, Kim, L.
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
;  FILE REFERENCE:  PM-0008-4 US
;  CURRENT APPLICATION NUMBER: US/09/596,002
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER:  60/140,121
;  PRIOR FILING DATE:  1999-06-18
;  NUMBER OF SEQ ID NOS:      41
;  SOFTWARE:      PERL Program
; SEQ ID NO 37
;   LENGTH: 99629
;   TYPE: DNA
;   ORGANISM: M. catarrhalis
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 78467
;   OTHER INFORMATION: a or g or c or t, unknown, or other
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte template ID No. 6632636 37
;  PUBLICATION INFORMATION:
US-09-596-002-37

Alignment Scores:
Pred. No.:                889           Length:          99629
Score:                    74.00         Matches:         31
Percent Similarity:       39.23%        Conservative:    20
Best Local Similarity:    23.85%        Mismatches:      52
Query Match:              10.66%        Indels:          27
DB:                       4             Gaps:            6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-596-002-37 (1-99629)

Qy         14 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysVal--- 32
Db       3115 AAGCTGTCACCATCAAAAAATCGCTGGCAGATTTTTCAACATTCAAACCCGTGCGTTGTA 3056

Qy         33 ------AsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIle 50
Db       3055 CTGTTTCAGGCAATGAACTCATGGCAGATTGTAATTTAT---------TTTGTACTTGTA 3005

Qy         51 TyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeu 70
Db       3004 CTTGGGCAG------------------TATCTGGATCAGTGCCATTTTCAA------ATG 2969

Qy         71 TyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGly 90
Db       2968 TTAAAGTCACAGAGGCAGACCCTGCCGCTGATGAATTTGATGACATGTACATCAGTCCAT 2909

Qy         91 -GlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsn---------- 106
Db       2908 CAATCCCTTTCATCTGCTGCTCGATGATCTGCGTGACCGAGTTTTCAACCGTCTCAGCAT 2849

Qy        107 ---------------SerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIleIl 121
Db       2848 CAGCACCTGGGTAGACGGCACGCACCTTTACTTGAGGCGGTGCAATTTTTGG-------- 2797

Qy        121 eLeuLeuAlaAsnProGlnPheIleSer 130
Db       2796 -GTATTGTTCAATCGGCAAATTATTAAT 2770


Search completed: April  7, 2004, 21:12:32
Job time : 76.9316 secs
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GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 18:25:49 ; Search time 204.104 Seconds
(without alignments)
2387.053 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FLQLETAKEPCMAKFGPLPS.....VLKNNTYWGIILLANPQFIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061640_2686/app_query.fasta_1.654
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09195368_@CGN_1_1_409_@runat_07042004_061640_2686
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 694 | 100.0 | 534 | 12 | US-10-202-062-39 | Sequence 39, Appl |
| 2 | 694 | 100.0 | 534 | 14 | US-10-272-411-9 | Sequence 9, Appli |
| 3 | 694 | 100.0 | 534 | 14 | US-10-218-547-39 | Sequence 39, Appl |
| 4 | 694 | 100.0 | 534 | 14 | US-10-272-328A-9 | Sequence 9, Appli |
| 5 | 694 | 100.0 | 534 | 14 | US-10-310-793-43 | Sequence 43, Appl |
| 6 | 694 | 100.0 | 1849 | 9 | US-09-345-790-1 | Sequence 1, Appli |
| 7 | 694 | 100.0 | 1849 | 13 | US-10-136-511-1 | Sequence 1, Appli |
| 8 | 694 | 100.0 | 1964 | 13 | US-10-080-455-2 | Sequence 2, Appli |
| 9 | 694 | 100.0 | 1964 | 13 | US-10-116-378-15 | Sequence 15, Appl |
| c 10 | 694 | 100.0 | 1964 | 13 | US-10-116-378-27 | Sequence 27, Appl |
| 11 | 107 | 15.4 | 60 | 10 | US-09-908-975-14130 | Sequence 14130, A |
| 12 | 92 | 13.3 | 50 | 15 | US-10-131-827-2732 | Sequence 2732, Ap |
| 13 | 83.5 | 12.0 | 1008 | 10 | US-09-951-061A-130 | Sequence 130, App |
| 14 | 80 | 11.5 | 3275 | 12 | US-10-205-331-15 | Sequence 15, Appl |
| 15 | 80 | 11.5 | 3275 | 15 | US-10-388-934-37 | Sequence 37, Appl |
| 16 | 78 | 11.2 | 474 | 14 | US-10-297-942-1 | Sequence 1, Appli |
| c 17 | 76 | 11.0 | 449 | 10 | US-09-918-995-2646 | Sequence 2646, Ap |
| 18 | 75.5 | 10.9 | 17388 | 9 | US-09-815-242-8512 | Sequence 8512, Ap |
| 19 | 75 | 10.8 | 474 | 14 | US-10-297-942-5 | Sequence 5, Appli |
| c 20 | 74.5 | 10.7 | 9524 | 14 | US-10-311-455-812 | Sequence 812, App |
| c 21 | 74.5 | 10.7 | 9524 | 16 | US-10-257-166-76 | Sequence 76, Appl |
| 22 | 74.5 | 10.7 | 13635 | 12 | US-10-210-175-13 | Sequence 13, Appl |
| 23 | 74.5 | 10.7 | 13635 | 16 | US-10-464-368-30 | Sequence 30, Appl |
| 24 | 74.5 | 10.7 | 14889 | 14 | US-10-101-510-356 | Sequence 356, App |
| 25 | 74.5 | 10.7 | 14896 | 15 | US-10-159-563-206 | Sequence 206, App |
| 26 | 74 | 10.7 | 474 | 14 | US-10-297-942-3 | Sequence 3, Appli |
| 27 | 74 | 10.7 | 2240 | 9 | US-09-757-041-1 | Sequence 1, Appli |
| 28 | 74 | 10.7 | 2339 | 14 | US-10-242-212-6 | Sequence 6, Appli |
| 29 | 74 | 10.7 | 2339 | 14 | US-10-207-655-102 | Sequence 102, App |
| 30 | 74 | 10.7 | 2359 | 8 | US-08-813-323A-3 | Sequence 3, Appli |
| 31 | 74 | 10.7 | 2455 | 8 | US-08-813-323A-4 | Sequence 4, Appli |
| 32 | 74 | 10.7 | 2455 | 14 | US-10-067-125-3 | Sequence 3, Appli |
| c 33 | 74 | 10.7 | 3153 | 12 | US-10-282-122A-26786 | Sequence 26786, A |
| c 34 | 74 | 10.7 | 4217 | 15 | US-10-369-493-27131 | Sequence 27131, A |
| 35 | 73 | 10.5 | 499 | 12 | US-10-085-783A-56227 | Sequence 56227, A |
| 36 | 73 | 10.5 | 499 | 15 | US-10-242-535A-56227 | Sequence 56227, A |
| 37 | 73 | 10.5 | 1545 | 14 | US-10-295-074-48 | Sequence 48, Appl |
| 38 | 73 | 10.5 | 1545 | 14 | US-10-295-074-50 | Sequence 50, Appl |
| 39 | 73 | 10.5 | 1545 | 14 | US-10-295-074-58 | Sequence 58, Appl |
| 40 | 73 | 10.5 | 1554 | 14 | US-10-295-074-52 | Sequence 52, Appl |
| c 41 | 72 | 10.4 | 345 | 12 | US-10-424-599-87615 | Sequence 87615, A |
| 42 | 72 | 10.4 | 477 | 14 | US-10-295-074-16 | Sequence 16, Appl |
| c 43 | 72 | 10.4 | 1203 | 10 | US-09-822-846-567 | Sequence 567, App |
| 44 | 72 | 10.4 | 1277 | 12 | US-10-425-114-1431 | Sequence 1431, Ap |
| c 45 | 72 | 10.4 | 1410 | 12 | US-10-424-599-106051 | Sequence 106051, |

ALIGNMENTS

RESULT 1
US-10-202-062-39
; Sequence 39, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 534
; TYPE: DNA
; ORGANISM: human
US-10-202-062-39

Alignment Scores:
Pred. No.: 3.9e-90 Length: 534
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     12             Gaps:          0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-202-062-39 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 2
US-10-272-411-9
; Sequence 9, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0202
;  CURRENT APPLICATION NUMBER: US/10/272,411
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/NM_005092.1
;   DATABASE ENTRY DATE: 2002-10-07
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AF125303.1
;   DATABASE ENTRY DATE: 1999-07-02
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AF117713.1
;   DATABASE ENTRY DATE: 1999-08-09
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AL031599.1
;   DATABASE ENTRY DATE: 1999-11-23
;   RELEVANT RESIDUES: (1)..(534)
US-10-272-411-9

Alignment Scores:
Pred. No.:              3.9e-90        Length:        534
Score:                  694.00         Matches:       130
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     14             Gaps:          0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-272-411-9 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 3
US-10-218-547-39
; Sequence 39, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Re
;  TITLE OF INVENTION:  Human Endokine Alpha
;  FILE REFERENCE: PF561
;  CURRENT APPLICATION NUMBER: US/10/218,547
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: 60/312,542
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: 60/330,761
;  PRIOR FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 534
;   TYPE: DNA
;   ORGANISM: human
US-10-218-547-39

Alignment Scores:
Pred. No.:              3.9e-90        Length:        534
Score:                  694.00         Matches:       130
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     14             Gaps:          0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-218-547-39 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531
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RESULT 4
US-10-272-328A-9
; Sequence 9, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-9

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 3.9e-90 | Length: | 534 |
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x US-10-272-328A-9 (1-534)

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Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531
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RESULT 5
US-10-310-793-43
; Sequence 43, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseas
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 534
; TYPE: DNA
; ORGANISM: human
US-10-310-793-43

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 3.9e-90 | Length: | 534 |
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x US-10-310-793-43 (1-534)

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Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
                |||||||||||||||||||||||||||||
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 6
US-09-345-790-1
; Sequence 1, Application US/09345790
; Patent No. US20020099198A1
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  Human Endokine Alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/345,790
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/912,227
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0470001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-09-345-790-1

Alignment Scores:
Pred. No.:              2.71e-89       Length:        1849
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|---|---|---|---|
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x US-09-345-790-1 (1-1849)

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Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
                |||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 7
US-10-136-511-1
; Sequence 1, Application US/10136511
; Publication No. US20020168729A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A.
;  TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
;  FILE REFERENCE: 1488.0470007/EKS/PSC
;  CURRENT APPLICATION NUMBER: US/10/136,511
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 09/513,584
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 09/345,790
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: 60/136,788
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/122,099
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: 08/912,227
;  PRIOR FILING DATE: 1997-08-15
;  PRIOR APPLICATION NUMBER: 60/024,058
;  PRIOR FILING DATE: 1996-08-16
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (53)..(559)
US-10-136-511-1

Alignment Scores:
Pred. No.:              2.71e-89       Length:        1849
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Score:                  694.00        Matches:       130
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     13            Gaps:          0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-136-511-1 (1-1849)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 8
US-10-080-455-2
; Sequence 2, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Mark, Melanie R.
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
;  FILE REFERENCE: P1150R2
;  CURRENT APPLICATION NUMBER: US/10/080,455
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: 09/195,368
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: US 60/069,661
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: US 60/065,635
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1857, 1875
;   OTHER INFORMATION: n may be any nucleotide
US-10-080-455-2

Alignment Scores:
Pred. No.:              2.98e-89      Length:        1964
Score:                  694.00        Matches:       130
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     13            Gaps:          0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-080-455-2 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 9
US-10-116-378-15
; Sequence 15, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 15
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1857, 1875
;   OTHER INFORMATION: n may be any nucleotide
US-10-116-378-15

Alignment Scores:
Pred. No.:              2.98e-89      Length:        1964
Score:                  694.00        Matches:       130
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     13            Gaps:          0
```

```
US-09-195-368-1_COPY_48_177 (1-130) x US-10-116-378-15 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
US-10-116-378-27/c
; Sequence 27, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 27
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 90, 108
;   OTHER INFORMATION: n may be any nucleotide
US-10-116-378-27

Alignment Scores:
Pred. No.:                2.98e-89        Length:         1964
Score:                    694.00          Matches:        130
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       13              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-116-378-27 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 1744

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 1684

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 1624

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 1564

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 1504

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 1444

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db       1443 ATTTTACTAGCAAATCCCCAATTCATCTCC 1414

RESULT 11
US-09-908-975-14130
; Sequence 14130, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/287,724
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/221,607
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14130
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-908-975-14130

Alignment Scores:
Pred. No.:                6.05e-07        Length:         60
Score:                    107.00          Matches:        20
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              15.42%          Indels:         0
DB:                       10              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x US-09-908-975-14130 (1-60)

Qy         25 AlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGln 44
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAGATACTTCAG 60

RESULT 12
US-10-131-827-2732
; Sequence 2732, Application US/10131827
; Publication No. US20040009479A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
;  TITLE OF INVENTION:  CHRONIC INFLAMMATORY DISEASES
;  FILE REFERENCE: 506612000120
;  CURRENT APPLICATION NUMBER: US/10/131,827
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9090
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-827-2732

Alignment Scores:
Pred. No.:              6.63e-05        Length:         50
Score:                  92.00           Matches:        16
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            13.26%          Indels:         0
DB:                     15              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-131-827-2732 (1-50)

Qy        104 IlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGly 119
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGT 50

RESULT 13
US-09-951-061A-130
; Sequence 130, Application US/09951061A
; Publication No. US20030082204A1
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Gettig, Russell
;    TITLE OF INVENTION:  POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
;    TITLE OF INVENTION:  RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
;    TITLE OF INVENTION:  RECOMBINANTS
;    NUMBER OF SEQUENCES:  143
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell, Boehnen, Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/951,061A
;      FILING DATE:  13-SEP-2001
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/354,138
;      FILING DATE:  15-JUL-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/224,657
;      FILING DATE:  16-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,962
;      FILING DATE:  08-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/776,867
;      FILING DATE:  23-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/621,614
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,283
;      FILING DATE:  31-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/621,614
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/713,967
;      FILING DATE:  11-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07,666,056
;      FILING DATE:  07-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2860
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1008 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-951-061A-130

Alignment Scores:
Pred. No.:              0.122           Length:         1008
Score:                  83.50           Matches:        31
Percent Similarity:     46.30%          Conservative:   19
Best Local Similarity:  28.70%          Mismatches:     34
Query Match:            12.03%          Indels:         24
DB:                     10              Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-951-061A-130 (1-1008)

Qy          2 LeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLys 21
              ||||||||||||          :::   ||:::   :::   |||   |||
Db        200 CTCCAATTGGAAGAACATTTGGATCGCTGCCTTTAGGAGTTGGGCGTACTACAGCCAGAC 259

Qy         22 TrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrp--------- 38
                :::           :::|||||||||                   |||
Db        260 CTGAGGAGTTATTGAAAGAAGCCACCCTGT-----------------TGGATATTATGG 301

Qy         39 ------LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaPro 56
                   :::|||:::::   :::|||      |||   |||        :::   |||
Db        302 TAAGGCGAACTGCAGGTGTCAAGGAACAACTGGTATTTTATA---------ATAACACCC 352

Qy         57 Asn-AlaAsnTyrAsnAspVal------AlaProPheGluValArgLeuTyrLysAsnLy 74
              ::: |||:::   |||   |||          |||:::|||   :::       :::   ||
Db        353 CATTGCACATCTTAACTCCGTGGAAAAAGGTCCTTACGAGTGGAAGTGTGTTCAGTGCAA 412

Qy         74 sAspMetIle--------------GlnThrLeuThrAsnLysSerLysIleGlnAsnVa 89
              |      :::              |||:::   :::   :::||||||||
Db        413 ATCAAGTCTGTAACACAGTCAATCTAATACCATTAGACATAGCACAAAGATTCAG----- 467

Qy         89 lGlyGlyThrTyrGluLeuHis 96
               ||||||   ||||||   |||
Db        468 -GGTGGTATATATGAGCATCAC 488
```

```
RESULT 14
US-10-205-331-15
; Sequence 15, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
;  APPLICANT: Warner-Lambert Company
;  APPLICANT:  Lee, Kevin
;  APPLICANT:  Dixon, Alistair
;  APPLICANT:  Brooksbank, Robert
;  APPLICANT:  Pinnock, Robert
;  TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
;  FILE REFERENCE: WL-A-018199
;  CURRENT APPLICATION NUMBER: US/10/205,331
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: GB 0118354.0
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 3275
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Cytosolic 3-hydroxy 3-methylglutaryl coenzyme A synthase
US-10-205-331-15

Alignment Scores:
Pred. No.:                2.46          Length:          3275
Score:                    80.00         Matches:         28
Percent Similarity:       43.97%        Conservative:    23
Best Local Similarity:    24.14%        Mismatches:      39
Query Match:              11.53%        Indels:          26
DB:                       12            Gaps:            5

US-09-195-368-1_COPY_48_177 (1-130) x US-10-205-331-15 (1-3275)

Qy         20 SerLysTrpGlnMetAlaSerSerGlu--------------ProProCysValAsnLys 34
              |||:::|||      ::::::   |||              ||||||   :::
Db       1458 TCAGAGTGGATGAAAAGCACAGAAGAACTTACGCCCGGCGTCCCTCCACAAATGACCACA 1517

Qy         35 Val------SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 52
              |||         :::|||   |||      :::|||       |||       |||
Db       1518 GTTTGGATGAAGGAGTGGGACTTG---TGCATTCAAACACAGCTACAGAGCATA------ 1568

Qy         53 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLys 72
                                                  |||:::   ||||||   |||
Db       1569 -------------------------------------TTCCAAGCCCGGCTAAGAAAG 1589

Qy         73 AsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThr 92
                :::|||   ::::::        |||   |||::::::   :::|||   |||:::
Db       1590 TGCCAAGACTTCCTGCGACCTCGGGCGAACCTGAGTCGGCTGTCATCAGTAACGGGGAGC 1649

Qy         93 TyrGlu---------LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHis 109
                |||         ||||||   |||      :::|||   ::::::   :::
Db       1650 ACTGAGAGCCGTGGCCTTCACAGAGGCTCGGGGCTGGATGGGGTATGGGAAACGTTAGAG 1709

Qy        110 GlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsn 125
              :::   :::      :::   :::         :::||||||   |||
Db       1710 GAATGGATGTCTTGGGACAATTTTACAGATTACGTGTTGCTTAAAAAT 1757

RESULT 15
US-10-388-934-37
; Sequence 37, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
;  APPLICANT: Boess, Franziska
;  APPLICANT:  Suter-Dick, Laura
;  APPLICANT:  Wolf, Detlef
;  TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
;  FILE REFERENCE: 21199
;  CURRENT APPLICATION NUMBER: US/10/388,934
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 02005336.9
;  PRIOR FILING DATE: 2002-03-14
;  PRIOR APPLICATION NUMBER: 02015657.6
;  PRIOR FILING DATE: 2002-07-17
;  NUMBER OF SEQ ID NOS: 862
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 3275
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-37

Alignment Scores:
Pred. No.:                2.46          Length:          3275
Score:                    80.00         Matches:         28
Percent Similarity:       43.97%        Conservative:    23
Best Local Similarity:    24.14%        Mismatches:      39
Query Match:              11.53%        Indels:          26
DB:                       15            Gaps:            5

US-09-195-368-1_COPY_48_177 (1-130) x US-10-388-934-37 (1-3275)

Qy         20 SerLysTrpGlnMetAlaSerSerGlu--------------ProProCysValAsnLys 34
              |||:::|||      ::::::   |||              ||||||   :::
Db       1458 TCAGAGTGGATGAAAAGCACAGAAGAACTTACGCCCGGCGTCCCTCCACAAATGACCACA 1517

Qy         35 Val------SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 52
              |||         :::|||   |||      :::|||       |||       |||
Db       1518 GTTTGGATGAAGGAGTGGGACTTG---TGCATTCAAACACAGCTACAGAGCATA------ 1568

Qy         53 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLys 72
                                                  |||:::   ||||||   |||
Db       1569 -------------------------------------TTCCAAGCCCGGCTAAGAAAG 1589

Qy         73 AsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThr 92
                :::|||   ::::::        |||   |||::::::   :::|||   |||:::
Db       1590 TGCCAAGACTTCCTGCGACCTCGGGCGAACCTGAGTCGGCTGTCATCAGTAACGGGGAGC 1649

Qy         93 TyrGlu---------LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHis 109
                |||         ||||||   |||      :::|||   ::::::   :::
Db       1650 ACTGAGAGCCGTGGCCTTCACAGAGGCTCGGGGCTGGATGGGGTATGGGAAACGTTAGAG 1709

Qy        110 GlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsn 125
              :::   :::      :::   :::         :::||||||   |||
Db       1710 GAATGGATGTCTTGGGACAATTTTACAGATTACGTGTTGCTTAAAAAT 1757


Search completed: April  8, 2004, 04:20:31
Job time : 218.104 secs
```

GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:53:26 ; Search time 231.205 Seconds
(without alignments)
2388.639 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FLQLETAKEPCMAKFGPLPS.....VLKNNTYWGIILLANPQFIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061637_2588/app_query.fasta_1.654
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09195368_@CGN_1_1_886_@runat_07042004_061637_2588 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 694 | 100.0 | 534 | 7 | ACC57580 | Acc57580 Polynucle |
| | 2 | 694 | 100.0 | 534 | 7 | ACC57909 | Acc57909 Human GIT |
| | 3 | 694 | 100.0 | 534 | 9 | ADC35221 | Adc35221 Human cDN |
| | 4 | 694 | 100.0 | 1809 | 2 | AAV19195 | Aav19195 Human end |
| | 5 | 694 | 100.0 | 1849 | 3 | AAA74936 | Aaa74936 cDNA enco |
| | 6 | 694 | 100.0 | 1849 | 3 | AAZ57314 | Aaz57314 Human end |
| | 7 | 694 | 100.0 | 1849 | 8 | ADA11463 | Ada11463 Human end |
| | 8 | 694 | 100.0 | 1849 | 9 | ADC01857 | Adc01857 Human cDN |
| | 9 | 694 | 100.0 | 1964 | 2 | AAX59844 | Aax59844 cDNA sequ |
| | 10 | 694 | 100.0 | 1964 | 2 | AAX87726 | Aax87726 Human PRO |
| | 11 | 694 | 100.0 | 1964 | 4 | AAC85435 | Aac85435 Clone PRO |
| | 12 | 694 | 100.0 | 1964 | 4 | AAF30051 | Aaf30051 Human cDN |
| | 13 | 694 | 100.0 | 1964 | 4 | AAC97374 | Aac97374 Human ang |
| | 14 | 694 | 100.0 | 1964 | 4 | AAC85945 | Aac85945 Native se |
| | 15 | 694 | 100.0 | 1964 | 4 | AAC90563 | Aac90563 Human PRO |
| | 16 | 694 | 100.0 | 1964 | 6 | ABK28562 | Abk28562 Human DNA |
| c | 17 | 566 | 81.6 | 1527 | 5 | AAS90614 | Aas90614 DNA encod |
| | 18 | 566 | 81.6 | 1527 | 5 | AAS81613 | Aas81613 DNA encod |
| | 19 | 107 | 15.4 | 60 | 6 | ABN41382 | Abn41382 Human spl |
| | 20 | 92 | 13.3 | 50 | 6 | ABZ02741 | Abz02741 Human leu |
| | 21 | 86 | 12.4 | 320 | 6 | ABN18154 | Abn18154 Human ORF |
| | 22 | 84.5 | 12.2 | 3666 | 9 | ADC90678 | Adc90678 E. faeciu |
| | 23 | 83.5 | 12.0 | 1008 | 6 | ABI98960 | Abi98960 Canine di |
| | 24 | 83.5 | 12.0 | 15690 | 6 | ABK15038 | Abk15038 Canine di |
| | 25 | 83.5 | 12.0 | 15690 | 6 | ABK15000 | Abk15000 Canine di |
| | 26 | 83.5 | 12.0 | 18826 | 6 | ABK15039 | Abk15039 Canine di |
| | 27 | 80 | 11.5 | 3275 | 8 | ACF25333 | Acf25333 Rat cytos |
| | 28 | 80 | 11.5 | 3275 | 9 | ADB58295 | Adb58295 Toxicity- |
| | 29 | 80 | 11.5 | 3275 | 9 | ADB52844 | Adb52844 Primary r |
| | 30 | 80 | 11.5 | 3977 | 2 | AAQ87698 | Aaq87698 Plasmid p |
| | 31 | 80 | 11.5 | 3977 | 2 | AAQ87699 | Aaq87699 Plasmid p |
| | 32 | 78.5 | 11.3 | 1797 | 6 | ABN66564 | Abn66564 Streptoco |
| c | 33 | 78.5 | 11.3 | 110000 | 6 | ABN71527_07 | Continuation (8 of |
| | 34 | 78 | 11.2 | 474 | 6 | ABA94384 | Aba94384 Human TNF |
| | 35 | 78 | 11.2 | 477 | 2 | AAV68423 | Aav68423 cDNA enco |
| | 36 | 77.5 | 11.2 | 1018 | 3 | AAA44544 | Aaa44544 Human sec |
| | 37 | 77 | 11.1 | 505 | 1 | AAN91642 | Aan91642 Synthetic |
| | 38 | 77 | 11.1 | 694 | 3 | AAC47600 | Aac47600 Arabidops |
| | 39 | 77 | 11.1 | 3977 | 2 | AAQ87696 | Aaq87696 Plasmid p |
| | 40 | 77 | 11.1 | 8298 | 2 | AAV18096 | Aav18096 pMCLDHAP |
| | 41 | 77 | 11.1 | 8543 | 2 | AAT47073 | Aat47073 Maize dwa |
| c | 42 | 76 | 11.0 | 449 | 8 | ACH15434 | Ach15434 Human adu |
| | 43 | 76 | 11.0 | 462 | 2 | AAQ03594 | Aaq03594 Encodes r |
| | 44 | 76 | 11.0 | 462 | 2 | AAQ02033 | Aaq02033 Sequence |
| | 45 | 76 | 11.0 | 3977 | 2 | AAQ87697 | Aaq87697 Plasmid p |

ALIGNMENTS

RESULT 1
ACC57580
ID ACC57580 standard; DNA; 534 BP.
XX
AC ACC57580;
XX
DT 28-JUL-2003 (first entry)
XX
DE Polynucleotide encoding tumour necrosis factor superfamily member.
XX
KW Human; RANKL; tumour necrosis factor; osteopathic; bone; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003033663-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033022.
XX
PR 15-OCT-2001; 2001US-0329393P.
XX
PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI Lam J, Ross PF, Teitelbaum SL;
XX
DR WPI; 2003-430346/40.
XX
PT New RANKL mimic comprising a core, and at least one external loop, useful
PT for enhancing processes of bone formation or inhibiting bone resorption,
PT thus providing treatments for disease or condition characterized by loss
PT of bone mass.

```
XX
PS   Disclosure; Page 58; 78pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a non-RANKL
CC   member of the tumour necrosis factor (TNF) superfamily. The invention
CC   provides non-naturally-occurring proteins that contain one or more of the
CC   external surface loops of RANKL (see ABR42066-70) in combination with a
CC   heterologous protein core obtained from a non-RANKL member of the TNF
CC   superfamily. Also provided are polynucleotides encoding such proteins.
CC   The proteins bind to RANK, acting as mimics of RANKL. They can be used to
CC   enhance bone formation by either inhibiting bone resorption or inducing
CC   osteogenesis, thus providing treatment for diseases or conditions
CC   characterised by loss of bone mass
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.01e-78        Length:          534
Score:                    694.00          Matches:         130
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       7               Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x ACC57580 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 2
ACC57909
ID   ACC57909 standard; cDNA; 534 BP.
XX
AC   ACC57909;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human GITRL polynucleotide.
XX
KW   Human; GITRL; tumour necrosis factor; ligand; cytostatic;
KW   immunomodulator; osteopathic; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .534
FT                   /*tag= a
FT                   /product= "Human GITRL"
XX
PN   WO2003040307-A2.
XX
PD   15-MAY-2003.
XX
PF   25-JUL-2002; 2002WO-US023782.
XX
PR   27-JUL-2001; 2001US-0307838P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Hilbert DH,  Rosen CA;
XX
DR   WPI; 2003-430659/40.
DR   P-PSDB; ABR42323.
XX
PT   New heteromultimeric complex having a first polypeptide member of the
PT   tumor necrosis factor (TNF) ligand family, and a second different member
PT   of TNF ligand family, useful for treating cancer, osteoporosis or an
PT   autoimmune disease.
XX
PS   Disclosure; Page 382; 388pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding human GITRL.
CC   The invention relates to compositions comprising heterotrimeric complexes
CC   of tumour necrosis factor (TNF) ligand family members, and their use in
CC   the detection, prevention and treatment of disease. In preferred
CC   embodiments, the heterotrimeric complex comprises full-length or
CC   extracellular portions of GITRL together with full-length or
CC   extracellular portions of other TNF ligand family members. The
CC   heterotrimeric complexes of the invention are useful for treating an
CC   autoimmune disease, cancer or osteoporosis, and particularly for
CC   inhibiting cancer cell proliferation, increasing B cell proliferation, or
CC   inducing apoptosis of T cells
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.01e-78        Length:          534
Score:                    694.00          Matches:         130
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       7               Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x ACC57909 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
```

```
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 3
ADC35221
ID   ADC35221 standard; cDNA; 534 BP.
XX
AC   ADC35221;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cDNA encoding TNF ligand family member #20.
XX
KW   ss; gene; human; tumour necrosis factor; TNF ligand; endokine alpha;
KW   excessive bone resorption disorder; osteoporosis; Paget's disease;
KW   arterial calcification.
XX
OS   Homo sapiens.
XX
PN   US2003100074-A1.
XX
PD   29-MAY-2003.
XX
PF   15-AUG-2002; 2002US-00218547.
XX
PR   16-AUG-2001; 2001US-0312542P.
PR   30-OCT-2001; 2001US-0330761P.
XX
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (NARD/) NARDELLI B.
XX
PI   Yu G,  Ni J,  Rosen CA,  Nardelli B;
XX
DR   WPI; 2003-696072/66.
DR   P-PSDB; ADC35222.
XX
PT   New Endokine alpha gene useful for preparing a composition for treating a
PT   disease associated with excessive or insufficient bone resorption e.g.,
PT   osteoporosis, Paget's disease or arterial calcification.
XX
PS   Disclosure; SEQ ID NO 39; 145pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule encoding a
CC   tumour necrosis factor family ligand. A composition comprising the
CC   isolated antibody or its fragment is used for treating an individual in
CC   need of decreased level of endokine alpha activity. The endokine alpha
CC   polypeptide present in a heterotrimeric complex is used for treating an
CC   individual having a disorder associated with excessive bone resorption,
CC   e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC   individual having a disorder associated with insufficient bone resorption
CC   comprises administering an endokine alpha antagonist, which is the
CC   antibody that binds specifically to endokine alpha polypeptide. The
CC   present sequence represents a cDNA encoding a tumour necrosis factor
CC   family ligand.
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.01e-78        Length:         534
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x ADC35221 (1-534)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 201

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 261

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 321

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 381

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 441

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        502 ATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 4
AAV19195
ID   AAV19195 standard; cDNA; 1809 BP.
XX
AC   AAV19195;
XX
DT   28-AUG-1998  (first entry)
XX
DE   Human endokine-alpha cDNA.
XX
KW   Endokine-alpha; cytokine; tumour necrosis factor; human;
KW   immunomodulation; infection; cell proliferation; angiogenesis; tumour;
KW   metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;
KW   diagnosis; therapy; ds; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
XX
PN   WO9807880-A1.
XX
PD   26-FEB-1998.
XX
PF   16-AUG-1996;   96WO-US013282.
XX
PR   16-AUG-1996;   96WO-US013282.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 1998-169182/15.
DR   P-PSDB; AAW37847.
XX
PT   Nucleic acid encoding human endokine-alpha - useful for diagnosis and
PT   treatment of tumour necrosis factor-related diseases.
XX
PS   Claim 1; Fig 1A-B; 78pp; English.
XX
CC   This isolated nucleic acid, deposited as ATCC 97640, codes for human
CC   endokine-alpha (see AAW37847), a novel member of the tumour necrosis
CC   factor (TNF) family of cytokines. It was isolated from a cDNA library
CC   established from human striatum. Expressed sequence tags corresponding to
CC   a portion of the endokine-alpha cDNA were also found in several
CC   endothelial libraries and a foetal liver library. Isolation of the
CC   nucleic acid allows production of recombinant endokine-alpha in
CC   transformed host cells. Endokine-alpha may be involved in disorders of
CC   immunomodulation, infection, cell proliferation, angiogenesis, tumour
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CC   metastasis, apoptosis, sepsis and endotoxaemia, and may be useful for
CC   treating melanoma and sarcoma. A claimed diagnostic method comprises
CC   assaying endokine-alpha gene expression as a means of detecting a TNF-
CC   related disorder. Fragments of endokinase-alpha nucleic acids can be used
CC   as probes, e.g. for fluorescent in situ hybridisation, for identifying
CC   genomic or other related sequences and in chromosome identification
XX
SQ   Sequence 1809 BP; 549 A; 355 C; 351 G; 554 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.67e-77        Length:         1809
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AAV19195 (1-1809)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        530 ATTTTACTGGCAAATCCCCAATTCATCTCC 559

RESULT 5
AAA74936
ID   AAA74936 standard; cDNA; 1849 BP.
XX
AC   AAA74936;
XX
DT   02-JAN-2001  (first entry)
XX
DE   cDNA encoding a human endokine-alpha polypeptide.
XX
KW   Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
KW   chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
KW   autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
KW   acute inflammation; acute allograft rejection; graft versus host disease;
KW   transplant rejection; foetal resorption; faecal peritonitis;
KW   bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemeia;
KW   polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
KW   chronic active hepatitis; myasthenia gravis; psoriasis; vitilogo;
KW   Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
KW   pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
KW   discoid lupus; dense deposit disease; endocrine ophthalmopathy;
KW   irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;
KW   juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
KW   lymphopenias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
KW   primary myxedema; polymyositis; mixed connective tissue disease;
KW   keratoconjunctivitis sicca; vernal keratoconjunctivitis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
FT                   /product= "endokine-alpha"
XX
PN   WO200050620-A2.
XX
PD   31-AUG-2000.
XX
PF   25-FEB-2000; 2000WO-US004722.
XX
PR   26-FEB-1999;   99US-0122099P.
PR   28-MAY-1999;   99US-0136788P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 2000-572097/53.
DR   P-PSDB; AAB08785.
XX
PT   Polynucleotide encoding endokine alpha protein, which is a member of
PT   tumor necrosis factor useful for treating inflammatory diseases,
PT   disorders such as cancer, allergy, diabetes and various neurological
PT   disorders.
XX
PS   Claim 5; Fig 1; 263pp; English.
XX
CC   The present sequence encodes a human endokine-alpha polypeptide. The
CC   polypeptide is a cytokine which is similar to tumour necrosis factor
CC   (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC   treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC   autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC   inflammation, acute inflammation, acute allograft rejection, graft versus
CC   host disease, transplant rejection, foetal resorption, faecal
CC   peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC   hypergammaglobulinemeia, polychondritis, scleroderma, Wegener
CC   granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC   gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitilogo,
CC   gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC   bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC   ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC   sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC   mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC   syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
CC   connective tissue disease, keratoconjunctivitis sicca, and vernal
CC   keratoconjunctivitis,
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.72e-77        Length:         1849
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AAA74936 (1-1849)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559
```

RESULT 6
AAZ57314
ID AAZ57314 standard; cDNA; 1849 BP.
XX
AC AAZ57314;
XX
DT 03-APR-2000 (first entry)
XX
DE Human endokine alpha protein encoding cDNA SEQ ID NO:1.
XX
KW Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KW immunomodulation; inflammation; cell proliferation; angiogenesis;
KW tumour metastasis; apoptosis; sepsis; endotoxemia; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 53. .562
FT /*tag= a
FT /product= "endokine alpha"
XX
PN US5998171-A.
XX
PD 07-DEC-1999.
XX
PF 15-AUG-1997; 97US-00912227.
XX
PR 16-AUG-1996; 96US-0024058P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Rosen CA, Yu G;
XX
DR WPI; 2000-104608/09.
DR P-PSDB; AAY53061.
XX
PT Isolated human endokine alpha gene useful as a diagnostic probes and
PT primers.
XX
PS Claim 3; Fig 1; 31pp; English.
XX
CC The present sequence encodes human endokine alpha which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC protein and polynucleotides can be used in diagnostic and therapeutic
CC methods concerning TNF family-related disorders. These include disorders
CC associated with immunomodulation and inflammation, cell proliferation,
CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
XX
SQ Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.72e-77 | Length: | 1849 |
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x AAZ57314 (1-1849)

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Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559
```

RESULT 7
ADA11463
ID ADA11463 standard; cDNA; 1849 BP.
XX
AC ADA11463;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human endokine alpha cDNA.
XX
KW human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;
KW infection; viral; bacterial; yeast; fungal; Toxoplasma gondii;
KW Schistosoma mansoni; Listeria monocytogenes; tumour necrosis factor;
KW TNF-related disorder; endokine alpha-related disorder; immunomodulation;
KW inflammation; cell proliferation; angiogenesis; tumour metastasis;
KW apoptosis; sepsis; endotoxaemia; ss; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 53. .562
FT /*tag= a
FT /product= "Endokine alpha"
XX
PN US2002099198-A1.
XX
PD 25-JUL-2002.
XX
PF 01-JUL-1999; 99US-00345790.
XX
PR 16-AUG-1996; 96US-0024058P.
PR 15-AUG-1997; 97US-00912227.
XX
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
XX
PI Yu G, Ni J, Rosen CA;
XX
DR WPI; 2003-605663/57.

```
DR   P-PSDB; ADA11464.
XX
PT   Novel isolated endokine alpha polypeptide, a member of tumor necrosis
PT   factor ligand family, and antibodies against the polypeptides, useful for
PT   treating melanoma, sarcoma, and viral, bacterial, fungal infections.
XX
PS   Claim 5; Fig 1; 29pp; English.
XX
CC   The invention relates to an isolated human endokine alpha polypeptide. A
CC   cell recombinant for the human endokine alpha polypeptide is useful for
CC   producing the protein by recombinant techniques. The antigenic epitope
CC   bearing peptides and polypeptides are useful to raise antibodies
CC   including monoclonal antibodies. The peptides and antipeptide antibodies
CC   are used in a variety of qualitative or quantitative assays for the
CC   protein. The protein is useful for tumour targeting and thus used in
CC   patients with melanoma and sarcoma for tumour regression and extension of
CC   patient life-span through a local injection. the protein is also useful
CC   for treating viral, bacterial, yeast, fungal and other infections e.g.,
CC   Toxoplasma gondii, Schistosoma mansoni, Listeria monocytogenes etc. The
CC   protein is also useful for treating other tumour necrosis factor (TNF)-
CC   related disorders. The nucleic acid is useful as probes for gene mapping
CC   by in situ hybridisation and for detecting expression of endokine alpha
CC   gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
CC   also useful for diagnosing an endokine alpha-related disorder such as
CC   disorders associated with immunomodulation and inflammation, cell
CC   proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
CC   endotoxaemia. The antibody is useful diagnostically or therapeutically as
CC   antagonists in the treatment of alpha and/or TNF-related disorders. The
CC   antibody is also useful for purification of the protein. The antibodies
CC   are useful for detecting the protein and for tracking the fate of various
CC   regions of a protein precursor which undergoes post-translational
CC   processing. The present sequence represents cDNA encoding human endokine
CC   alpha.
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.72e-77      Length:          1849
Score:                  694.00        Matches:         130
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     8             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x ADA11463 (1-1849)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559
```

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RESULT 8
ADC01857
ID   ADC01857 standard; cDNA; 1849 BP.
XX
AC   ADC01857;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cDNA encoding Endokine alpha.
XX
KW   Human; ss; gene; endokine alpha; tumour necrosis factor family; AIDS;
KW   chronic lymphocyte disorder; tumour; parasitic disease;
KW   autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
KW   graft versus host disease; transplant rejection; skin allergy;
KW   bowel disease; wound; sepsis; Hodgkin's disease;
KW   chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;
KW   chronic active hepatitis; myasthenia gravis; psoriasis;
KW   autoimmune thyroiditis; Goodpasture's disease; asthma; Graves disease;
KW   cirrhosis; insulin dependent diabetes mellitus; Sjogren's syndrome;
KW   glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
KW   rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
FT                   /product= "Endokine alpha"
XX
PN   US2002168729-A1.
XX
PD   14-NOV-2002.
XX
PF   02-MAY-2002; 2002US-00136511.
XX
PR   16-AUG-1996;   96US-0024058P.
PR   15-AUG-1997;   97US-00912227.
PR   26-FEB-1999;   99US-0122099P.
PR   28-MAY-1999;   99US-0136788P.
PR   01-JUL-1999;   99US-00345790.
PR   25-FEB-2000; 2000US-00513584.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 2003-755028/71.
XX
PT   Novel isolated endokine alpha polypeptide AIDS, chronic lymphocyte
PT   disorder, common variable immunodeficiency, a tumor, parasitic disease,
PT   autoimmune disease, lupus, arthritis, multiple sclerosis.
XX
PS   Claim 1; SEQ ID NO 1; 90pp; English.
XX
CC   The invention relates to an isolated endokine alpha polypeptide (a member
CC   of the tumour necrosis factor family), appearing as ADC01858, the
CC   sequence of the endokine alpha polypeptide having an sequence encoded by
CC   the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
CC   sequence of an epitope-bearing portion of the above polypeptides. Also
CC   included are the encoding nucleic acid (its homologues, complements or
CC   fragments where the fragment comprises at least 50 contiguous
CC   nucleotides), provided that the fragment is not from a region starting at
CC   nucleotide 26 and ending at nucleotide 476 of ADC01857), making a
CC   recombinant vector comprising the nucleic acid and an isolated antibody
CC   or antibody fragment that binds specifically to endokine alpha. The DNA
CC   and protein are useful for treating an individual having a disorder
CC   chosen from AIDS, chronic lymphocyte disorder, common variable
CC   immunodeficiency, a tumour, parasitic disease, autoimmune disease, lupus,
CC   arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
CC   chronic inflammation, acute inflammation, acute allograft rejection,
CC   graft versus host disease, transplant rejection, foetal resorption,
CC   faecal peritonitis, skin allergies, bowel disease, a wound, sepsis, ALL,
```

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CC   Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocyte leukaemia,
CC   plasmacytomas, multiple myeloma, Burkitt's lymphoma, EBV-transformed
CC   disease, chronic myelogenous leukaemia, chronic hypergammaglobulinaemeia,
CC   autoimmune haematological disorders, polychondritis, scleroderma, Wegener
CC   granulomatosis, dermatomyosisitis, chronic active hepatitis, myasthenia
CC   gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, autoimmune
CC   thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
CC   enteropathy, autoimmune neutropenias, pemphigus vulgaris, Goodpasture's
CC   disease, bullous pemphigoid, discoid lupus, dense deposit disease,
CC   endocrine ophthalmopathy, IBD, asthma, Graves disease, Sarcoidosis,
CC   cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
CC   uveitis, autoimmune gastritis, lymphopaenias, olyarteritis nodosa,
CC   Sjogren's syndrome, Bechet's disease, Hashimoto's disease, primary
CC   myxedema, polymyositis, mixed connective tissue disease,
CC   keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
CC   lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
CC   anaemia, contact sensitivity disease, Parkinson's disease, primary
CC   lateral sclerosis, silicosis, sarcoidosis, idiopathic pulmonary fibrosis,
CC   idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis,
CC   histamine-mediated allergic reactions, IgE-mediated allergic reactions,
CC   rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
CC   present sequence encodes Endokine alpha.
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.72e-77      Length:          1849
Score:                    694.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       9             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x ADC01857 (1-1849)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 9
AAX59844
ID   AAX59844 standard; cDNA; 1964 BP.
XX
AC   AAX59844;
XX
DT   28-JUL-1999  (first entry)
XX
DE   cDNA sequence for human DNA19355.
XX
KW   DNA19355; tumour necrosis factor homologue; receptor GITR; immunogen;
KW   antibody; apoptosis; mammalian cancer cell;
KW   tumour necrosis factor (TNF)-alpha secretion; primary T- cell;
KW   proinflammatory response; ds.
XX
OS   Homo sapiens.
XX
PN   WO9925834-A1.
XX
PD   27-MAY-1999.
XX
PF   18-NOV-1998;   98WO-US024621.
XX
PR   18-NOV-1997;   97US-0065635P.
PR   12-DEC-1997;   97US-0069661P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti R,  Baker KP;
PI   Godowski PJ,  Mark MR;
XX
DR   WPI; 1999-338009/28.
DR   P-PSDB; AAY15817.
XX
PT   New DNA19355 polypeptide as tumour necrosis factor homolog.
XX
PS   Example 1; Fig 1; 86pp; English.
XX
CC   The present sequence encodes a polypeptide designated DNA19355. The
CC   polypeptide is a tumour necrosis factor homologue. The DNA19355
CC   polynucleotide sequence can be used to derive hybridisation probes for
CC   e.g. isolating similar sequences, gene mapping, genetic analysis, etc.
CC   Nucleic acids which encode DNA19355 can also be used to generate
CC   transgenic or knockout animals, which are useful in the development and
CC   screening of therapeutically useful reagents. The DNA19355 polypeptides
CC   may be used in diagnostic assays to detect the presence of the receptor
CC   GITR in mammalian tissues. The polypeptides can also be used as
CC   immunogens to raise antibodies. The polypeptides may also be used to
CC   induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
CC   stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
CC   cells, and so can be used to stimulate a proinflammatory response in
CC   mammalian cells
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                1.87e-77      Length:          1964
Score:                    694.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       2             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AAX59844 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
AAX87726
ID   AAX87726 standard; cDNA; 1964 BP.
XX
AC   AAX87726;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human PRO364 ligand cDNA clone DNA19355-1150..
XX
KW   PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
KW   inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
KW   therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             21. .554
FT                   /*tag=  a
XX
PN   WO9940196-A1.
XX
PD   12-AUG-1999.
XX
PF   09-FEB-1999;   99WO-US002642.
XX
PR   09-FEB-1998;   98US-0074087P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti RM,  Wood WI;
PI   Goddard A;
XX
DR   WPI; 1999-494296/41.
DR   P-PSDB; AAY06646.
XX
PT   Tumor necrosis factor receptor homologue - useful for, e.g. modulating
PT   apoptosis and NF-KB activation and proinflammatory or autoimmune
PT   responses.
XX
PS   Example 2; Fig 5A-B; 104pp; English.
XX
CC   This is the nucleotide sequence of a novel cDNA clone, termed DNA19355-
CC   1150 (ATCC 209466), coding for a potential ligand (see AAY06646) of
CC   PRO384 (see AAY06605), a novel member of the tumour necrosis factor
CC   receptor family. The clone was isolated from a human umbilical vein
CC   endothelial cell cDNA library constructed in yeast transformants. PRO364
CC   polypeptides are useful for modulating apoptosis, NF-KB activation and
CC   proinflammatory or autoimmune responses in mammalian cells (claimed)
XX
SQ   Sequence 1964 BP; 596 A; 370 C; 380 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              1.87e-77        Length:         1964
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AAX87726 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 11
AAC85435
ID   AAC85435 standard; cDNA; 1964 BP.
XX
AC   AAC85435;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Clone PRO175-1150.
XX
KW   PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW   hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR;
KW   human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW   myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW   age-related macular degeneration; antibody; periodontal disease;
KW   vascular-related drug targeting; atherosclerosis; hypertension;
KW   inflammatory vasculitides; Reynaud's disease; aneurysm;
KW   arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
KW   fibrosis; neuropathy; rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             21. .554
FT                   /*tag=  a
FT                   /product= "PRO175"
XX
PN   WO200103720-A2.
XX
PD   18-JAN-2001.
XX
PF   11-JUL-2000; 2000WO-US018867.
XX
PR   12-JUL-1999;   99US-0143304P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Williams PM,  Gerritsen ME;
XX
DR   WPI; 2001-138257/14.
DR   P-PSDB; AAB47056.
XX
PT   Composition for diagnosing and treating cardiovascular, endothelial and
PT   angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX
PS   Example 2; Fig 5; 76pp; English.
```

```
XX
CC   This sequence encodes a PRO175 polypeptide, which is a human gluco-
CC   corticoid-induced tumor necrosis factor ligand (hGITRL). The
CC   corresponding receptor (hGITR), PRO364, is given in AAB47054. PRO364 and
CC   PRO175 may be used in a mixture with a cardiovascular, endothelial,
CC   angiogenic or angiostatic agent for the treatment of a cardiovascular,
CC   endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was
CC   isolated from an expressed sequence tag (EST) database as having homology
CC   to members of the tumour necrosis factor receptor (TNFR) family of
CC   polypeptides. The PRO175 cDNA sequence was isolated from a library of
CC   cDNA fragments derived from human umbilical vein endothelial cells
CC   (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
CC   antagonists is useful for treating cardiac hypertrophy (which is
CC   initiated by myocardial infarction and characterized by the presence of
CC   an elevated level of PGF_2alpha), trauma, a cancer, or age-related
CC   macular degeneration in a human. Administering a therapeutically
CC   effective amount of an antibody that binds PRO364 or PRO175 is useful for
CC   inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
CC   from a tumor or a retinal disorder. PRO364 or PRO175, or their
CC   antagonists, are useful for vascular-related drug targeting or as
CC   therapeutic targets for the treatment or prevention of atherosclerosis,
CC   hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
CC   arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
CC   or regeneration and treatment of lung or liver fibrosis, periodontal
CC   diseases, attraction of bone-forming cells, central and peripheral
CC   nervous system disease and neuropathies and rheumatoid arthritis
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                1.87e-77      Length:          1964
Score:                    694.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AAC85435 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 12
AAF30051
ID   AAF30051 standard; cDNA; 1964 BP.
XX
AC   AAF30051;
XX
DT   30-APR-2001  (first entry)
XX
DE   Human cDNA encoding PRO175.
XX
KW   PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;
KW   antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW   antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW   dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW   immunostimulant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             21. .554
FT                   /*tag=  a
FT   sig_peptide     21. .152
FT                   /*tag=  b
FT   mat_peptide     153. .551
FT                   /*tag=  c
XX
PN   WO200105972-A1.
XX
PD   25-JAN-2001.
XX
PF   15-MAR-2000; 2000WO-US006884.
XX
PR   20-JUL-1999;   99US-0144758P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Fong S,  Goddard A,  Godowski PJ;
PI   Gurney AL,  Hillan KJ,  Mark MR,  Marsters SA,  Pitti RM,  Tumas D;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-103149/11.
DR   P-PSDB; AAB20109.
XX
PT   New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT   diagnosing and treating immune-related disorders, such as multiple
PT   sclerosis, rheumatoid arthritis and diabetes.
XX
PS   Claim 21; Fig 3; 127pp; English.
XX
CC   The present sequence is that of cDNA clone DNA19355-1150 (ATCC 209466)
CC   encoding novel human immunomodulator protein PRO175 (UNQ149) (see
CC   AAB20109). The clone was isolated from a yeast screening of human cDNA.
CC   The predicted protein (20 kDa, pI 8.08) shows homology to members of the
CC   tumour necrosis factor family. The invention provides polynucleotides
CC   (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
CC   including PRO175. Claimed compositions comprising these proteins or their
CC   agonists are useful for increasing infiltration of inflammatory cells
CC   into a tissue of a mammal, stimulating or enhancing an immune response in
CC   a mammal, or increasing the proliferation of T-lymphocytes in a mammal in
CC   response to an antigen. Claimed compositions comprising the PRO
CC   polypeptide or its antagonist have the opposite effect. A claimed method
CC   for treating an immune related disorder, such as a T cell disorder,
CC   involves administering the PRO polypeptide, an agonist antibody or an
CC   antagonist antibody. The disorder is selected from systemic lupus
CC   erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC   arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
CC   inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC   sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC   thyroiditis, diabetes mellitus, immune-mediated renal disease,
CC   demyelinated diseases (such as multiple sclerosis), autoimmune chronic
CC   active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,
CC   sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis
CC   and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,
CC   (auto)immune-mediated skin diseases (such as bullous skin disease,
CC   erythema multiforme and psoriasis), allergic diseases (such as asthma,
CC   allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC   urticaria), immunologic diseases of the lung and transplantation
CC   associated diseases (such as graft rejection and graft-versus-host
CC   disease) (all claimed). Claimed methods of diagnosing these disorders
```

CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies, and a method of stimulating an immune response in a mammal
CC using PRO179
XX
SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.87e-77 | Length: | 1964 |
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x AAF30051 (1-1964)

```
Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551
```

RESULT 13
AAC97374
ID AAC97374 standard; cDNA; 1964 BP.
XX
AC AAC97374;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO175 cDNA, SEQ ID NO:8.
XX
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
PF 05-JAN-2000; 2000WO-US000219.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR P-PSDB; AAB53065.
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiogenic
PT disorders, such as atherosclerosis, wounds or cancer.
XX
PS Claim 58; Fig 3A-B; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to screen
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
CC therapy. PRO nucleic acids can also be used to produce transgenic animals
CC useful for the development and screening of potential therapeutic agents.
CC The present sequence represents a cDNA encoding a PRO protein of the
CC invention
XX
SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.87e-77 | Length: | 1964 |
| Score: | 694.00 | Matches: | 130 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

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US-09-195-368-1_COPY_48_177 (1-130) x AAC97374 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 14
AAC85945
ID   AAC85945 standard; cDNA; 1964 BP.
XX
AC   AAC85945;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Native sequence of PRO175 cDNA, clone DNA19355-1150-1.
XX
KW   PRO; type II transmembrane protein; tumour necrosis factor; stroke;
KW   heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;
KW   myocardial infarction; cardiac hypertrophy; PGF_2alpha; trauma; bone;
KW   cancer; age-related macular degeneration; wound; burn; hypertension;
KW   diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
KW   rheumatoid arthritis; Crohn's disease; amylotrophic lateral sclerosis;
KW   endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             16. .554
FT                   /*tag=  a
FT                   /product= "PRO175 polypeptide"
FT   sig_peptide     16. .95
FT                   /*tag=  b
FT   mat_peptide     96. .551
FT                   /*tag=  c
XX
PN   WO200140464-A1.
XX
PD   07-JUN-2001.
XX
PF   11-AUG-2000; 2000WO-US022031.
XX
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   05-JAN-2000; 2000WO-US000219.
PR   24-FEB-2000; 2000WO-US005004.
PR   15-MAR-2000; 2000WO-US006884.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   30-MAY-2000; 2000WO-US014941.
PR   28-JUL-2000; 2000WO-US020710.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Godowski PJ,  Gurney AL;
PI   Hillan KJ,  Mark MR,  Marsters SA,  Paoni NF,  Pitti RM,  Wood WI;
XX
DR   WPI; 2001-381383/40.
DR   P-PSDB; AAB47287.
XX
PT   Isolated PRO polypeptide useful in treating and diagnosing a
PT   cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes
PT   mellitus, myocardial infarction, arthritis.
XX
PS   Claim 57; Fig 1; 144pp; English.
XX
CC   The sequences given in AAC85945-48 encode PRO polypeptides. PRO175 shows
CC   type II transmembrane protein typology, and portions of PRO364 show
CC   homology to members of the tumour necrosis factor (TNF) family, thereby
CC   indicating that it may be a novel member of the TNF family. PRO175 and
CC   PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a
CC   compound that inhibits PRO, diagnosing a cardio- vascular, endothelial or
CC   angiogenic disorder in a mammal by detecting PRO cDNA, treating
CC   cardiovascular, endothelial or angiogenic disorder in a mammal, and
CC   inducing cardiac hypertrophy or inhibiting endothelial cell growth or
CC   angiogenesis in a mammal. The mammal is a human which has suffered
CC   myocardial infarction, cardiac hypertrophy characterized by the presence
CC   of elevated PGF_2alpha, trauma, cancer or age-related macular
CC   degeneration. Trauma includes wounds or burns. Other treatable diseases
CC   include diabetes mellitus, osteoporosis, ischaemia, hypertension,
CC   rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
CC   endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
CC   repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC   amylotrophic lateral sclerosis, and stroke
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                1.87e-77        Length:          1964
Score:                    694.00          Matches:         130
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       4               Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AAC85945 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
```

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                    ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 15
AAC90563
ID   AAC90563 standard; cDNA; 1964 BP.
XX
AC   AAC90563;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO175 cDNA.
XX
KW   Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW   vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW   vulnerary; antianginal; gene therapy; cardiovascular disease;
KW   endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW   wound healing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073445-A2.
XX
PD   07-DEC-2000.
XX
PF   17-MAY-2000; 2000WO-US013705.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Kuo SS,  Mark MR,  Marsters SA;
PI   Paoni NF,  Pitti RM,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-025251/03.
DR   P-PSDB; AAB50951.
XX
PT   Seventeen nucleic acids encoding PRO polypeptides which are useful in
PT   diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT   disorders in a mammal.
XX
PS   Claim 60; Fig 1; 182pp; English.
XX
CC   The present sequence is one of seventeen nucleic acids encoding PRO
CC   polypeptides. The PRO nucleic acids, polypeptides, agonists and
CC   antagonists are useful for treating cardiovascular, endothelial or
CC   angiogenic disorders in a mammal. Examples of these disorders include
CC   cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis
CC   and lymphangitis. The PRO polypeptides and antagonists are also used to
CC   prevent tumour angiogenesis and for treating periodontal diseases. They
CC   are also used to stimulate wound healing and tissue regeneration. The PRO
CC   nucleic acids, polypeptides and anti-PRO antibodies are useful for
CC   diagnosing a cardiovascular, endothelial or angiogenic disorder
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              1.87e-77        Length:         1964
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AAC90563 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

Search completed: April  7, 2004, 17:08:51
Job time : 236.205 secs
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GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 16:50:59 ; Search time 1779.77 Seconds
(without alignments)
2181.225 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FLQLETAKEPCMAKFGPLPS.....VLKNNTYWGIILLANPQFIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061638_2606/app_query.fasta_1.654
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 694 | 100.0 | 634 | 13 | BX473859 | BX473859 DKFZp686K |
| 2 | | 608 | 87.6 | 669 | 29 | AG182677 | AG182677 Pan trogl |
| 3 | | 294 | 42.4 | 350 | 13 | BY216375 | BY216375 BY216375 |
| 4 | | 240 | 34.6 | 348 | 13 | BY214208 | BY214208 BY214208 |
| 5 | | 138 | 19.9 | 334 | 13 | BY326400 | BY326400 BY326400 |
| 6 | | 127 | 18.3 | 328 | 13 | BY326606 | BY326606 BY326606 |
| 7 | | 123 | 17.7 | 324 | 13 | BY327839 | BY327839 BY327839 |
| 8 | c | 117 | 16.9 | 114 | 29 | CG977950 | CG977950 CH240_168 |
| 9 | | 110 | 15.9 | 727 | 13 | BU294618 | BU294618 603603621 |
| 10 | | 110 | 15.9 | 731 | 13 | BU373331 | BU373331 603589056 |
| 11 | | 88 | 12.7 | 638 | 9 | AI982044 | AI982044 pat.pk007 |
| 12 | | 87.5 | 12.6 | 855 | 13 | BX843917 | BX843917 BX843917 |
| 13 | c | 85 | 12.2 | 575 | 13 | BW232049 | BW232049 BW232049 |
| 14 | | 85 | 12.2 | 878 | 29 | CG463627 | CG463627 ZUAHK11TV |
| 15 | | 84.5 | 12.2 | 814 | 28 | BZ758026 | BZ758026 PUDBK49TD |
| 16 | c | 84 | 12.1 | 564 | 13 | BW091647 | BW091647 BW091647 |
| 17 | c | 84 | 12.1 | 566 | 9 | AV895903 | AV895903 AV895903 |
| 18 | c | 84 | 12.1 | 682 | 9 | AV854531 | AV854531 AV854531 |
| 19 | c | 84 | 12.1 | 694 | 9 | AV894346 | AV894346 AV894346 |
| 20 | | 84 | 12.1 | 720 | 13 | BW299761 | BW299761 BW299761 |
| 21 | c | 84 | 12.1 | 726 | 13 | BW169798 | BW169798 BW169798 |
| 22 | c | 84 | 12.1 | 728 | 13 | BW169887 | BW169887 BW169887 |
| 23 | c | 84 | 12.1 | 729 | 13 | BW169841 | BW169841 BW169841 |
| 24 | c | 84 | 12.1 | 746 | 13 | BW175773 | BW175773 BW175773 |
| 25 | c | 84 | 12.1 | 771 | 13 | BW062488 | BW062488 BW062488 |
| 26 | c | 83 | 12.0 | 470 | 9 | AI168441 | AI168441 ok30g08.x |
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| 28 | | 82.5 | 11.9 | 602 | 13 | BW305081 | BW305081 BW305081 |
| 29 | c | 82.5 | 11.9 | 800 | 12 | BG246328 | BG246328 602355119 |
| 30 | c | 82 | 11.8 | 358 | 10 | BF121624 | BF121624 601757130 |
| 31 | | 81.5 | 11.7 | 973 | 28 | BZ967128 | BZ967128 PUDDS30TD |
| 32 | c | 81.5 | 11.7 | 1059 | 14 | CK027902 | CK027902 AGENCOURT |
| 33 | | 81 | 11.7 | 625 | 29 | AG247887 | AG247887 Lotus cor |
| 34 | | 81 | 11.7 | 771 | 13 | BX862196 | BX862196 BX862196 |
| 35 | c | 79.5 | 11.5 | 516 | 14 | CA785834 | CA785834 sat39h05. |
| 36 | | 79.5 | 11.5 | 829 | 14 | CB292943 | CB292943 UCRCS01_0 |
| 37 | c | 79.5 | 11.5 | 843 | 29 | CC988505 | CC988505 ZUACM68TV |
| 38 | c | 79 | 11.4 | 397 | 13 | BY075703 | BY075703 BY075703 |
| 39 | c | 79 | 11.4 | 417 | 12 | BI006601 | BI006601 MR1-RT003 |
| 40 | | 79 | 11.4 | 417 | 12 | BM001637 | BM001637 1031097E0 |
| 41 | | 79 | 11.4 | 550 | 9 | AV394317 | AV394317 AV394317 |
| 42 | c | 79 | 11.4 | 642 | 29 | CC877676 | CC877676 ZMMBBb021 |
| 43 | | 79 | 11.4 | 656 | 28 | AZ869907 | AZ869907 2M0182O07 |
| 44 | | 79 | 11.4 | 734 | 9 | AI055157 | AI055157 coau0003D |
| 45 | c | 79 | 11.4 | 735 | 29 | CG737137 | CG737137 ZMMBBb032 |

ALIGNMENTS

RESULT 1
BX473859
LOCUS BX473859 634 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686K13165_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686K13165 5', mRNA sequence.
ACCESSION BX473859
VERSION BX473859.1 GI:31668103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 634)

```
  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686K13165) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .634
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686K13165"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Alignment Scores:
Pred. No.:              7.43e-76        Length:         634
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     13              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x BX473859 (1-634)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 245

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 305

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 365

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 425

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 485

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 545

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        546 ATTTTACTAGCAAATCCCCAATTCATCTCC 575

RESULT 2
AG182677
LOCUS       AG182677                669 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-055O22.T7, genomic survey
            sequence.
ACCESSION   AG182677
VERSION     AG182677.1  GI:16712357
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-055O22.T7"
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ORIGIN

Alignment Scores:
Pred. No.:              4.17e-65        Length:         669
Score:                  608.00          Matches:        114
Percent Similarity:     95.04%          Conservative:   1
Best Local Similarity:  94.21%          Mismatches:     6
Query Match:            87.61%          Indels:         0
DB:                     29              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AG182677 (1-669)

Qy         10 ProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluPro 29
              ||||||:::  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CCTTGTATATTTCTTACAGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCT 317

Qy         30 ProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeu 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTA 377

Qy         50 IleTyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArg 69
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        378 ATTTATGGCCAAGTGGCTCCCAATGCAAACTACAATGATGTAGTTCCTTTTGAGGTGCGG 437

Qy         70 LeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnVal 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CTGTATAAAAACAAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTA 497

Qy         90 GlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHis 109
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        498 GGAGGGACTTATGAATTGCATGTTGGGGACACCATAGACTAGATATTTAACTCTGAGCAT 557

Qy        110 GlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIle 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        558 CAGGTTCTAAAAAATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAACTTATT 617
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Qy        130 Ser 130
              |||
Db        618 TCC 620

RESULT 3
BY216375
LOCUS       BY216375                350 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY216375 RIKEN full-length enriched, activated spleen Mus musculus
            cDNA clone F830044F01 5', mRNA sequence.
ACCESSION   BY216375
VERSION     BY216375.1  GI:26397123
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 350)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .350
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="NOD"
                      /db_xref="taxon:10090"
                      /clone="F830044F01"
                      /tissue_type="activated spleen"
                      /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:
Pred. No.:                2.07e-26        Length:          350
Score:                    294.00          Matches:         62
Percent Similarity:       65.49%          Conservative:    12
Best Local Similarity:    54.87%          Mismatches:      37
Query Match:              42.36%          Indels:          2
DB:                       13              Gaps:            2

US-09-195-368-1_COPY_48_177 (1-130) x BY216375 (1-350)

Qy          6 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 25
              ||||||   |||   ||||||   ||||||           |||||||||   |||
Db         10 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 69

Qy         26 SerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsn 45
              |||   :::|||   |||||||||       ||||||   ||||||:::|||||||||:::
Db         70 TCTCCCAAACCTCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGT 129

Qy         46 GlyLeuTyrLeuIleTyrGlyGlnValAlaPro---AsnAlaAsnTyr---AsnAspVal 63
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Db        130 GGCACATATTTAATCTACGGCCAAGTGATTCCTGTGGATAAGAAATACATAAAAGACAAT 189

Qy         64 AlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLys 83
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Db        190 GCCCCCTTCGTAGTACAGATATATAAAAAGAATGATGTCCTACAAACTCTAATGAATGAT 249

Qy         84 SerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeu 103
              :::|||     :::||||||   ||||||||||||   |||||  |||   |||
Db        250 TTTCAAATCTTGCCTATAGGAGGGGTTTATGAACTGCATGCTGGAGATAACATATATCTG 309

Qy        104 IlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 116
                |||||||||:::      :::   |||   ||||||
Db        310 AAGTTCAACTCTAAAGACCATATTCAGAAAACTAACACA 348

RESULT 4
BY214208
LOCUS       BY214208                348 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY214208 RIKEN full-length enriched, activated spleen Mus musculus
            cDNA clone F830027N19 5', mRNA sequence.
ACCESSION   BY214208
VERSION     BY214208.1  GI:26394920
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
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            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NOD"
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ORIGIN

Alignment Scores:
Pred. No.:                1.1e-19        Length:          348
Score:                    240.00         Matches:         60
Percent Similarity:       62.28%         Conservative:    11
Best Local Similarity:    52.63%         Mismatches:      40
Query Match:              34.58%         Indels:          4
DB:                       13             Gaps:            2

US-09-195-368-1_COPY_48_177 (1-130) x BY214208 (1-348)

Qy          6 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 25
              ||||||   |||  ||||||  ||||||            |||||||||   |||
Db         10 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 69

Qy         26 SerSerGluProProCysValAsnLysValSerAsp-TrpLysLeuGluIleLeuGlnAs 45
                ||:::        ||||||       ||||||    ||||||:::|||||||||::
Db         70 TC-TCCCAAACTCAATGGGTGAATACGACATCTGATGGGGAAGCTGAAGATACTGCAGAG 128

Qy         45 nGlyLeuTyrLeuIleTyrGlyGlnValAlaPro---AsnAlaAsnTyr---AsnAspVa 63
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Db        129 TGGCACATATTTAATCTACGGCCAAGTGATTCCTGTGGATAAGAAATACATAAAAGACAA 188

Qy         63 lAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLy 83
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Qy         83 sSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLe 103
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Db        249 TTTTCAAATCTTGCCTATAGGAGGGGTTTATGAACTGCATGCTGGAGATAACATATATCT 308

Qy        103 uIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 116
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Db        309 GAAGTTCAACTCTAAAGACCATANTCAGAAAACTAACACA 348

RESULT 5
BY326400
LOCUS       BY326400                334 bp    mRNA    linear   EST 11-DEC-2002
DEFINITION  BY326400 RIKEN full-length enriched, synovial fibroblasts Mus
            musculus cDNA clone L030036A22 5', mRNA sequence.
ACCESSION   BY326400
VERSION     BY326400.1  GI:26516959
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
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            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
```

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .334
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030036A22"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 5.25e-07 | Length: | 334 |
| Score: | 138.00 | Matches: | 28 |
| Percent Similarity: | 67.39% | Conservative: | 3 |
| Best Local Similarity: | 60.87% | Mismatches: | 15 |
| Query Match: | 19.88% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x BY326400 (1-334)

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Qy          6 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 25
              ||||||   |||  ||||||  ||||||           |||||||||   |||
Db        195 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 254

Qy         26 SerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsn 45
                 |||   :::|||   |||||||||      ||||||  ||||||:::|||||||||:::
Db        255 TCTCCCAAACCTCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGT 314

Qy         46 GlyLeuTyrLeuIleTyr 51
                ||| |||||||||||||
Db        315 GGCACATATTTAATCTAC 332
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RESULT 6
BY326606
LOCUS BY326606 328 bp mRNA linear EST 11-DEC-2002
DEFINITION BY326606 RIKEN full-length enriched, synovial fibroblasts Mus musculus cDNA clone L030037A06 5', mRNA sequence.
ACCESSION BY326606
VERSION BY326606.1 GI:26517167
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 328)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .328
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030037A06"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

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|---|---|---|---|
| Pred. No.: | 1.2e-05 | Length: | 328 |
| Score: | 127.00 | Matches: | 26 |
| Percent Similarity: | 65.91% | Conservative: | 3 |
| Best Local Similarity: | 59.09% | Mismatches: | 15 |
| Query Match: | 18.30% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-09-195-368-1_COPY_48_177 (1-130) x BY326606 (1-328)

```
Qy          6 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 25
              ||||||   |||   ||||||   ||||||           |||||||||   |||
Db        195 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 254

Qy         26 SerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsn 45
              |||   :::|||   ||||||||          ||||||   ||||||:::|||||||||:::
Db        255 TCTCCCAAACCTCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGT 314

Qy         46 GlyLeuTyrLeu 49
              |||   ||||||
Db        315 GGCACATATTTA 326
```

RESULT 7
BY327839
LOCUS BY327839 324 bp mRNA linear EST 11-DEC-2002
DEFINITION BY327839 RIKEN full-length enriched, synovial fibroblasts Mus musculus cDNA clone L030044D24 5', mRNA sequence.
ACCESSION BY327839
VERSION BY327839.1 GI:26518410
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .324
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030044D24"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:
Pred. No.: 3.71e-05 Length: 324

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Score:                  123.00          Matches:        25
Percent Similarity:     65.12%          Conservative:   3
Best Local Similarity:  58.14%          Mismatches:     15
Query Match:            17.72%          Indels:         0
DB:                     13              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x BY327839 (1-324)

Qy          6 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 25
              ||||||   |||   ||||||   ||||||             |||||||   |||
Db        195 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 254

Qy         26 SerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsn 45
              |||   :::|||   |||||||||      ||||||   ||||||:::||||||||:::
Db        255 TCTCCCAAACCTCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGT 314

Qy         46 GlyLeuTyr 48
              |||   |||
Db        315 GGCACATAT 323

RESULT 8
CG977950/c
LOCUS       CG977950                 114 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  CH240_168J10.TV CHORI-240 Bos taurus genomic clone CH240_168J10,
            genomic survey sequence.
ACCESSION   CG977950
VERSION     CG977950.1  GI:39903729
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 114)
  AUTHORS   Costa,J.N., Mota,M. and Caetano,A.R.
  TITLE     Brazil's Contribution to End-Sequencing the Bovine BAC Library
            CHORI-240
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: CH240_168J10.TJ
            Contact: Caetano AR
            Department of Biotechnology
            Embrapa Recursos Geneticos e Biotecnologia
            Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
            02372, 70770-900 Brasil
            Tel: 55 61 448 4778
            Fax: 55 61 340 3658
            Email: acaetano@cenargen.embrapa.br
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm).
             Bases shown have Phred quality value equal to or higher then 20.
            Bases with quality value below 20 were masked with 'N'.
             For BAC library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org).
             Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm).
             This work was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
            Biotecnologia with financing from Conselho Nacional de
            Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
            Plate: 168  row: J  column: 10
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 114.
FEATURES             Location/Qualifiers
     source          1. .114
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_168J10"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:              4.34e-05        Length:         114
Score:                  117.00          Matches:        19
Percent Similarity:     85.19%          Conservative:   4
Best Local Similarity:  70.37%          Mismatches:     4
Query Match:            16.86%          Indels:         0
DB:                     29              Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x CG977950 (1-114)

Qy         16 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 35
              ||||||||||||||||||||||||||||||   |||   ||||||   |||:::||||||
Db         81 GGACCATTACCTTCAAAATGGCAAATGCCTTCTCCTGAGCCTTCTTGTATGAATAAGACA 22

Qy         36 SerAspTrpLysLeuGluIle 42
              :::||||||:::|||:::|||
Db         21 GCTGACTGGAGGCTGAAGATA 1

RESULT 9
BU294618
LOCUS       BU294618                 727 bp    mRNA    linear   EST 27-NOV-2002
DEFINITION  603603621F1 CSEQCHN55 Gallus gallus cDNA clone ChEST582i6 5', mRNA
            sequence.
ACCESSION   BU294618
VERSION     BU294618.1  GI:25744254
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 727)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .727
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST582i6"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN55"
                     /note="Organ: kidney + adrenal; Vector: pBluescript II
                     KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
                     library was constructed from 1 million independent clones.
                     cDNA synthesis was initiated using an oligo(dT) primer,
                     using methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
```

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 0.00517 | Length: | 727 |
| Score: | 110.00 | Matches: | 38 |
| Percent Similarity: | 48.03% | Conservative: | 23 |
| Best Local Similarity: | 29.92% | Mismatches: | 46 |
| Query Match: | 15.85% | Indels: | 20 |
| DB: | 13 | Gaps: | 6 |

US-09-195-368-1_COPY_48_177 (1-130) x BU294618 (1-727)

```
Qy         15 PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLys 34
              |||   |||:::      ||||||   |||   :::|||       |||       :::
Db        184 TTCTCCCCAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCCAACGAGCAGCTTG 237

Qy         35 ValSer------AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 52
              :::|||      :::  ||||||::::::   :::   ||||||||   ||||||
Db        238 ATATCCTACCATGAGGGGAAGCTGAAGGTGGAGAAAGCAGGGCTCTACTACATCTACTCA 297

Qy         53 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr--- 71
              ||||||:::                ||||||||   :::   :::|||
Db        298 CAAGTCAGCTTCTGCACCAAGGCGGCGGCTTCGGCGCCATTCACCCTCTATATTTATTTG 357

Qy         72 --------------------------------LysAsnLysAspMetIleGlnThrLeu 80
                                              |||       |||       |||
Db        358 TACCTCCCCATGGAAGAGGACCGGCTCCTGATGAAGGGACTTGACACGCACAGCACCTCC 417

Qy         81 ThrAsnLysSerLysIleGlnAsnVal------GlyGlyThrTyrGluLeuHisValGly 98
              |||         ::::::|||::::::      ||||||   :::||||||      |||
Db        418 ACGGCTCTCTGTGAGCTCCAGTCCATCCGGGAGGGCGGTGTCTTCGAGCTGCGGCAGGGC 477

Qy         99 AspThr------IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 116
              |||         :::::::::      ::::::         |||       ||||||
Db        478 GACATGGTCTTTGTCAATGTGACGGACTCAACAGCAGTGAACGTCAACCCTGGCAACACC 537

Qy        117 TyrTrpGlyIleIleLeuLeu 123
              |||:::|||:::      |||
Db        538 TACTTTGGCATGTTCAAGCTG 558
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RESULT 10
BU373331

```
LOCUS       BU373331                731 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603589056F1 CSEQCHN74 Gallus gallus cDNA clone ChEST549p13 5', mRNA
            sequence.
ACCESSION   BU373331
VERSION     BU373331.1  GI:25881332
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST549p13"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN74"
                     /note="Organ: kidney + adrenal; Vector: pBluescript II
                     KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
                     library was constructed from 1 million independent clones.
                     cDNA synthesis was initiated using an oligo(dT) primer,
                     using methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN
```

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 0.00522 | Length: | 731 |
| Score: | 110.00 | Matches: | 38 |
| Percent Similarity: | 48.03% | Conservative: | 23 |
| Best Local Similarity: | 29.92% | Mismatches: | 46 |
| Query Match: | 15.85% | Indels: | 20 |
| DB: | 13 | Gaps: | 6 |

US-09-195-368-1_COPY_48_177 (1-130) x BU373331 (1-731)

```
Qy         15 PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLys 34
              |||   |||:::      ||||||   |||   :::|||       |||       :::
Db        186 TTCTCCCCAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCCAACGAGCAGCTTG 239

Qy         35 ValSer------AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 52
              :::|||      :::  ||||||::::::   :::   ||||||||   ||||||
Db        240 ATATCCTACCATGAGGGGAAGCTGAAGGTGGAGAAAGCAGGGCTCTACTACATCTACTCA 299

Qy         53 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr--- 71
              ||||||:::                ||||||||   :::   :::|||
Db        300 CAAGTCAGCTTCTGCACCAAGGCGGCGGCTTCGGCGCCATTCACCCTCTATATTTATTTG 359

Qy         72 --------------------------------LysAsnLysAspMetIleGlnThrLeu 80
                                              |||       |||       |||
Db        360 TACCTCCCCATGGAAGAGGACCGGCTCCTGATGAAGGGACTTGACACGCACAGCACCTCC 419

Qy         81 ThrAsnLysSerLysIleGlnAsnVal------GlyGlyThrTyrGluLeuHisValGly 98
              |||         ::::::|||::::::      ||||||   :::||||||      |||
Db        420 ACGGCTCTCTGTGAGCTCCAGTCCATCCGGGAGGGCGGTGTCTTCGAGCTGCGGCAGGGC 479

Qy         99 AspThr------IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 116
              |||         :::::::::      ::::::         |||       ||||||
Db        480 GACATGGTCTTTGTCAATGTGACGGACTCAACAGCAGTGAACGTCAACCCTGGCAACACC 539

Qy        117 TyrTrpGlyIleIleLeuLeu 123
              |||:::|||:::      |||
Db        540 TACTTTGGCATGTTCAAGCTG 560
```

RESULT 11
AI982044

```
LOCUS       AI982044                638 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
            clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION   AI982044
VERSION     AI982044.1  GI:5885072
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 638)
AUTHORS Tirunagaru,V.G., Sofer,L., Cui,J. and Burnside,J.
TITLE An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones
JOURNAL Genomics 66 (2), 144-151 (2000)
MEDLINE 20318616
PUBMED 10860659
COMMENT Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@UDel.Edu, www.chickest.udel.edu
Seq primer: T7.
FEATURES Location/Qualifiers
source 1. .638
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pat.pk0072.c9.f"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F'"
/clone_lib="chicken activated T cell cDNA"
/note="Vector: pcDNA3"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.34 | Length: | 638 |
| Score: | 88.00 | Matches: | 28 |
| Percent Similarity: | 45.74% | Conservative: | 15 |
| Best Local Similarity: | 29.79% | Mismatches: | 35 |
| Query Match: | 12.68% | Indels: | 16 |
| DB: | 9 | Gaps: | 3 |

US-09-195-368-1_COPY_48_177 (1-130) x AI982044 (1-638)

```
Qy         46 GlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaPro 65
              |||||||||   ||||||   ||||||:::                          ||||||
Db          3 GGGCTCTACTACATCTACTCACAAGTCAGCTTCTGCACCAAGGCGGCGGCTTCGGCGCCA 62

Qy         66 PheGluValArgLeuTyr-----------------------------------LysAsn 73
              |||   :::   :::|||                                     |||
Db         63 TTCACCCTCTATATTTATTTGTACCTCCCCATGGAAGAGGACCGGCTCCTGATGAAGGGA 122

Qy         74 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnVal------GlyGly 91
                 |||          |||   |||          ::::::|||::::::      ||||||
Db        123 CTTGACACGCACAGCACCTCCACGGCTCTCTGTGAGCTCCAGTCCATCCGGGAGGGCGGT 182

Qy         92 ThrTyrGluLeuHisValGlyAspThr------IleAspLeuIlePheAsnSerGluHis 109
              :::||||||      ||||||         :::::::::     ::::::
Db        183 GTCTTCGAGCTGCGGCAGGGCGACATGGTCTTTGTCAATGTGACGGACTCAACAGCAGTG 242

Qy        110 GlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeu 123
                 |||       |||||||||:::|||:::      |||
Db        243 AACGTCAACCCTGGCAACACCTACTTTGGCATGTTCAAGCTG 284
```

RESULT 12
BX843917
LOCUS BX843917 855 bp mRNA linear EST 11-DEC-2003
DEFINITION BX843917 Xenopus laevis unfertilized egg cDNA library Xenopus laevis cDNA clone IMAGp998J159020 ; IMAGE:3744110 5', mRNA sequence.
ACCESSION BX843917
VERSION BX843917.1 GI:39743018
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 855)
AUTHORS Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D., Schroth,A., Korn,B. and Landgrebe,J.
TITLE Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998J159020.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB No.998) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: m13r, 5' TTTCACACAGGAAACAGCTATGAC 3'.
FEATURES Location/Qualifiers
source 1. .855
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGp998J159020 ; IMAGE:3744110"
/tissue_type="unfertilized egg"
/lab_host="Top-10 F'"
/clone_lib="Xenopus laevis unfertilized egg cDNA library"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; This library has been used successfully to clone a number of full-length cDNAs ranging in size from 1.4 to 4.5 kb. There are less than 0.5% clones with multiple inserts. Since each cDNA has an EcoRI site at its 5' end and an XhoI site at the 3' end, these clones can be easily identified. One should be suspicious of any clone which gives 3 or more bands in an EcoRI-XhoI double digest AND has an internal XhoI site. We usually do not further characterize any such clones unless the cDNA is known to give multiple bands in an EcoRI-XhoI digest. Microplate status: 500,000 unamplified cDNAs were mass excised (pBluescript SK-) in X11-Blue using ExAssist phage. The resulting single-stranded phagemids were used to infect Top10F'. Clones were picked into freezing medium (per liter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM K2HPO4, 13.2 mM KH2PO4, 1.7 mM Na-citrate, 0.4 mM MgSO4*7 H2O, 6.8 mM (NH4)2SO4, 4% w/v glycerol) and grown for 24 hours. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC) library"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 4.19 | Length: | 855 |
| Score: | 87.50 | Matches: | 41 |
| Percent Similarity: | 35.88% | Conservative: | 20 |
| Best Local Similarity: | 24.12% | Mismatches: | 54 |
| Query Match: | 12.61% | Indels: | 55 |
| DB: | 13 | Gaps: | 8 |

US-09-195-368-1_COPY_48_177 (1-130) x BX843917 (1-855)

```
Qy          3 GlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrp 22
              |||   :::                 |||   :::|||         :::    |||
Db        264 CAGTTCCAAGTGGGAAATGCTAGAACTGAGGCATGGTATGGGTCGAGGAACAACAGCTGG 323

Qy         23 GlnMetAla-----------------------------SerSerGluProProCysVal 32
                 :::|||                            :::||||||         |||
```

```
Db        324 CCAGTTGCTCATCTTACTGTTGGGAATATTACACCTAGTAACAGTGAACAGTCAAAGGTG 383

Qy         33 Asn-------------------------------------------------LysValSer 36
                |||                                                   |||
Db        384 AACCTTACTTTCTGGAATATCCGAGAAGGTTGGGCAAATCTGAGAAACATAAAGTACCAT 443

Qy         37 AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly------------ 52
               :::  ||||||||||||||||||:::|||   |||  :::|||
Db        444 AACGGAAAGCTGGAAATCTTACAAGATGGCTATTACTTTGTATATGCAAATCTGTGCTTT 503

Qy         53 ------GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeu 70
                     :::                 |||  |||  |||      ::::::  :::
Db        504 AGACACCATATACATAAAGGAAAAGAATACCGAGACAAGGCT---CTGCAGCTTATGATG 560

Qy         71 Tyr--------------LysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLys 85
              |||              ||||||:::          :::||||||           |||
Db        561 TACATCTGTAAAGCAAGCAAGAACAGGAGGCCTTATGAAACGCTAATGAAGGGAGGGAAA 620

Qy         86 IleGln-----------------------------------------AsnValGlyGlyThr 92
                                                             ||||||
Db        621 ACTGCCATTTGGTCAAATAATTCAGTCTATCACTTTTATTCTGTATATAAAGGAGGGGTT 680

Qy         93 TyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeu 112
              ::::::||||||   ||||||   |||      |||      |||      ::::::|||
Db        681 TTTAAATTACATGCTGGTGATCAGATA---TTCATCCAAGCTTCCTATTTAGAACTGTTG 737

Qy        113 ---------LysAsnAsnThrTyrTrpGly 119
                     :::      ||||||:::|||
Db        738 GACCCAGCACAAGAAGCTACATATTTTGGG 767

RESULT 13
BW232049/c
LOCUS       BW232049                575 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  BW232049 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad101c12 5', mRNA sequence.
ACCESSION   BW232049
VERSION     BW232049.1  GI:24753614
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 575)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .575
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad101c12"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

Alignment Scores:
Pred. No.:              4.74          Length:          575
Score:                  85.00         Matches:         28
Percent Similarity:     43.64%        Conservative:    20
Best Local Similarity:  25.45%        Mismatches:      36
Query Match:            12.25%        Indels:          26
DB:                     13            Gaps:            5
```

```
US-09-195-368-1_COPY_48_177 (1-130) x BW232049 (1-575)

Qy         40 LeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsn 59
              ::::::||||||::::::|||||||||  ||||||  ||||||          |||
Db        515 ATCAAAATTCTGGAGAGCGGACTTTACTACATTTACGCGCAGGTAACATACCGCGCAACA 456

Qy         60 TyrAsnAspValAlaPro-----------------PheGluValArgLeuTyrLysAsn 73
                         |||||||||               ||||||:::|||:::      :::
Db        455 AGAACACGTGTTGCACCTTGGAATGGACAAGTGTTGTTTGAAATACGGATGACGGACGAT 396

Qy         74 ---LysAspMetIleGlnThrLeuThr--------------------AsnLysSerLys 85
                 |||:::   :::      |||                      :::   ::::::
Db        395 CNCCCGGATTTATTTGAACCAACAACAACGACCTTATTGAGATCATTNTCACATACAAGG 336

Qy         86 IleGlnAsn--------------------------ValGlyGlyThrTyrGluLeuHis 96
                 |||                           :::||||||          ||||||
Db        335 GCCATGAACACCACTCCTGTCCCAGAATNTGGTTATTTAGGTGGCTTACAAAGATTACAC 276

Qy         97 ValGlyAspThrIleAspLeuIlePheAsnSer---------GluHisGlnValLeuLys 113
              |||     |||  :::      ::::::      :::  :::
Db        275 GCCGGTCAAGTTATTTTNGTGCATGAGAGCACNCCGATGCGAAGGTACAGTATGCAACCG 216

Qy        114 AsnAsnThrTyrTrpGlyIleIleLeuLeu 123
                    |||:::|||      |||:::
Db        215 ACGGAAAATTACTTTGGCGCATTCCTGGTC 186

RESULT 14
CG463627
LOCUS       CG463627                878 bp    DNA     linear   GSS 17-SEP-2003
DEFINITION  ZUAHK11TV ZM_3.0_4.0_KB Zea mays genomic clone ZMMBPa0070A21,
            genomic survey sequence.
ACCESSION   CG463627
VERSION     CG463627.1  GI:34848627
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: ZUAHK11TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .878
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBPa0070A21"
                     /clone_lib="ZM_3.0_4.0_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
                     genomic DNA library"
ORIGIN

Alignment Scores:
Pred. No.:              8.93          Length:          878
Score:                  85.00         Matches:         26
Percent Similarity:     43.33%        Conservative:    13
Best Local Similarity:  28.89%        Mismatches:      27
Query Match:            12.25%        Indels:          24
DB:                     29            Gaps:            3
```

```
US-09-195-368-1_COPY_48_177 (1-130) x CG463627 (1-878)

Qy          12 MetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCys 31
               :::      |||||||||          |||   :::      |||         |||
Db         655 CTAGGCACTTTTGGACCA---------AAGTGCAAATATCAAAGTAAAAGAGCACCTTAA 705

Qy          32 ValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyr 51
                  |||   :::|||   ||||||:::      |||   :::|||::::::   :::|||
Db         706 ACCAACTATCTTTCACATTGGAAAATTTGCAAGTTGAATAGTGGAATTTGG---GTCTAC 762

Qy          52 GlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr 71
                  |||   ||||||:::      |||
Db         763 TTGCAAAAAGCACCCCATAAACCATAT-------------------------------- 789

Qy          72 LysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGly 91
                                                |||||:::||||||   :::|||
Db         790 -------------------------ATGCCTAAGTCTGAAATTCAGTGCATGGGGTCA 822

Qy          92 ThrTyrGluLeuHisValGlyAspThrIle 101
               |||   ||||||::::::      |||
Db         823 ACTTTGGAGCTCTATATCTCTCAATTCATA 852

RESULT 15
BZ758026
LOCUS       BZ758026                814 bp    DNA     linear   GSS 10-MAR-2003
DEFINITION  PUDBK49TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa149I01,
            genomic survey sequence.
ACCESSION   BZ758026
VERSION     BZ758026.1  GI:28911400
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 814)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUDBK49TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .814
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa149I01"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

Alignment Scores:
Pred. No.:              9.2          Length:         814
Score:                  84.50        Matches:        34
Percent Similarity:     39.34%       Conservative:   14
Best Local Similarity:  27.87%       Mismatches:     29
Query Match:            12.18%       Indels:         45
DB:                     28           Gaps:           6

US-09-195-368-1_COPY_48_177 (1-130) x BZ758026 (1-814)

Qy          12 MetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCys 31
               :::      |||||||||          |||   :::      |||         |||
Db         225 CTAGGCACTTTTGGACCA---------AAGCGCAAATATCAAAGTAAAAGAGCACCTTAA 275

Qy          32 ValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyr 51
                  |||   :::|||   |||::::::      |||   :::|||::::::      |||
Db         276 ACCAACTATCTTTCATATTGGAGAATTTGCAAGTTGAATAGTGGAATTTGG---GCCTAC 332

Qy          52 GlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr 71
                  |||   ||||||:::      |||
Db         333 ATGCAAAAAGCACCCCATAAACCATAT-------------------------------- 359

Qy          72 LysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGly 91
                                                |||||:::||||||   :::|||
Db         360 -------------------------ATGCCTAAGTCTGAAATTCAGTGCATAGGGTCA 392

Qy          92 ThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnVal 111
               |||   ||||||::::::                                     |||
Db         393 ACTTTGGAGCTCTATATCTCT---------------------------------CAATTC 419

Qy         112 LeuLysAsn-----------AsnThr----------------TyrTrpGlyIleIle 121
               :::||||||           ||||||                |||   ||||||
Db         420 ATAAAGAATTTGCCCTAGGTCAACACATCAAGGTTATAGAGCTACTATAGGGGCATAACT 479

Qy         122 LeuLeu 123
               ||||||
Db         480 TTGCTT 485

Search completed: April  7, 2004, 19:35:59
Job time : 1791.77 secs
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GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:55:16 ; Search time 1941.11 Seconds
(without alignments)
2902.773 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FLQLETAKEPCMAKFGPLPS.....VLKNNTYWGIILLANPQFIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061638_2594/app_query.fasta_1.654
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09195368_@CGN_1_1_5417_@runat_07042004_061638_2594 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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21: em_or:*
22: em_ov:*
23: em_pat:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 694 | 100.0 | 510 | 9 | AF117713 | AF117713 Homo sapi |
| 2 | 694 | 100.0 | 534 | 9 | AF125303 | AF125303 Homo sapi |
| 3 | 694 | 100.0 | 1849 | 6 | AR092586 | AR092586 Sequence |
| 4 | 694 | 100.0 | 1849 | 6 | BD268764 | BD268764 Human end |
| 5 | 694 | 100.0 | 1849 | 6 | AR214043 | AR214043 Sequence |
| 6 | 694 | 100.0 | 1849 | 6 | AR282586 | AR282586 Sequence |
| 7 | 694 | 100.0 | 1964 | 6 | AX074393 | AX074393 Sequence |
| 8 | 694 | 100.0 | 1964 | 6 | AX077015 | AX077015 Sequence |
| 9 | 694 | 100.0 | 1964 | 6 | AX080755 | AX080755 Sequence |
| 10 | 694 | 100.0 | 1964 | 6 | AX150805 | AX150805 Sequence |
| 11 | 694 | 100.0 | 1964 | 6 | AX391258 | AX391258 Sequence |
| 12 | 694 | 100.0 | 1964 | 6 | BD085993 | BD085993 Tumor nec |
| 13 | 694 | 100.0 | 1964 | 6 | BD124038 | BD124038 Novel tum |
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| 16 | 628 | 90.5 | 163136 | 9 | HS15D23 | AL031599 Human DNA |
| 17 | 348 | 50.1 | 568 | 10 | AY234223 | AY234223 Mus muscu |
| 18 | 348 | 50.1 | 1261 | 10 | MMU577580 | AJ577580 Mus muscu |
| 19 | 348 | 50.1 | 2066 | 10 | MMU577579 | AJ577579 Mus muscu |
| 20 | 344 | 49.6 | 522 | 10 | AY267900 | AY267900 Mus muscu |
| 21 | 342 | 49.3 | 522 | 10 | AY359852 | AY359852 Mus muscu |
| 22 | 342 | 49.3 | 528 | 10 | AY320040 | AY320040 Mus muscu |
| 23 | 325 | 46.8 | 228107 | 2 | AC109057 | AC109057 Rattus no |
| 24 | 315 | 45.4 | 116159 | 2 | AC117819 | AC117819 Mus muscu |
| 25 | 108.5 | 15.6 | 892 | 5 | GGA243435 | AJ243435 Gallus ga |
| 26 | 91 | 13.1 | 183800 | 2 | BX629345 | BX629345 Danio rer |
| 27 | 91 | 13.1 | 197642 | 2 | BX530057 | BX530057 Danio rer |
| 28 | 90 | 13.0 | 187859 | 2 | BX323804 | BX323804 Danio rer |
| 29 | 90 | 13.0 | 193788 | 2 | BX323559 | BX323559 Danio rer |
| 30 | 89 | 12.8 | 225126 | 2 | AC138679 | AC138679 Mus muscu |
| c 31 | 88 | 12.7 | 182818 | 5 | BX649257 | BX649257 Zebrafish |
| 32 | 87 | 12.5 | 136581 | 9 | AC008459 | AC008459 Homo sapi |
| c 33 | 87 | 12.5 | 137324 | 2 | AC010459 | AC010459 Homo sapi |
| c 34 | 87 | 12.5 | 141591 | 9 | AC079467 | AC079467 Homo sapi |
| c 35 | 87 | 12.5 | 157122 | 9 | AC079015 | AC079015 Homo sapi |
| c 36 | 87 | 12.5 | 162162 | 2 | AC012432 | AC012432 Homo sapi |
| c 37 | 87 | 12.5 | 162705 | 9 | AC099493 | AC099493 Homo sapi |
| c 38 | 87 | 12.5 | 174086 | 2 | AC110010 | AC110010 Homo sapi |
| 39 | 87 | 12.5 | 186922 | 2 | BX470115 | BX470115 Danio rer |
| c 40 | 87 | 12.5 | 194215 | 2 | AC024422 | AC024422 Homo sapi |
| c 41 | 86.5 | 12.5 | 153751 | 3 | AC116551 | AC116551 Dictyoste |
| 42 | 86 | 12.4 | 183797 | 9 | AC022400 | AC022400 Homo sapi |
| c 43 | 86 | 12.4 | 198218 | 2 | AC037447 | AC037447 Homo sapi |
| 44 | 86 | 12.4 | 207120 | 2 | AL844520 | AL844520 Homo sapi |
| c 45 | 86 | 12.4 | 234248 | 2 | AC119385 | AC119385 Rattus no |

ALIGNMENTS

RESULT 1

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AF117713
LOCUS       AF117713                 510 bp    mRNA    linear   PRI 09-MAR-1999
DEFINITION  Homo sapiens AITR ligand (TL6) mRNA, complete cds.
ACCESSION   AF117713
VERSION     AF117713.1  GI:4378801
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Kwon,B., Yu,K.Y., Ni,J., Yu,G.L., Jang,I.K., Kim,Y.J., Xing,L.,
            Liu,D., Wang,S.X. and Kwon,B.S.
  TITLE     Identification of a novel activation-inducible protein of the tumor
            necrosis factor receptor superfamily and its ligand
  JOURNAL   J. Biol. Chem. 274 (10), 6056-6061 (1999)
  MEDLINE   99156876
   PUBMED   10037686
REFERENCE   2  (bases 1 to 510)
  AUTHORS   Kwon,B., Yu,K.Y., Ni,J. and Kwon,B.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-1999) Micro. & Immunol., Indiana University, 635
            Barnhill Dr., Indianapolis, IN 46202, USA
FEATURES             Location/Qualifiers
     source          1. .510
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="endothelial cell"
     gene            1. .510
                     /gene="TL6"
     CDS             1. .510
                     /gene="TL6"
                     /codon_start=1
                     /product="AITR ligand"
                     /protein_id="AAD19695.1"
                     /db_xref="GI:4378802"
                     /translation="MPLSHSRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFIFLQLE
                     TAKEPCMAKFGPLPSKWQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVAPNANYNDV
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                     LLANPQFIS"
ORIGIN

Alignment Scores:
Pred. No.:              2.45e-69        Length:         510
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AF117713 (1-510)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Db        118 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 177

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 237

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 297

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Db        298 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 357

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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Db        478 ATTTTACTGGCAAATCCCCAATTCATCTCC 507

RESULT 2
AF125303
LOCUS       AF125303                 534 bp    mRNA    linear   PRI 02-APR-1999
DEFINITION  Homo sapiens glucocorticoid-induced TNFR-related protein ligand
            (TNFSF18) mRNA, complete cds.
ACCESSION   AF125303
VERSION     AF125303.1  GI:4558500
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Gurney,A.L., Marsters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
  TITLE     Identification of a new member of the tumor necrosis factor family
            and its receptor, a human ortholog of mouse GITR
  JOURNAL   Curr. Biol. (1999) In press
REFERENCE   2  (bases 1 to 534)
  AUTHORS   Gurney,A.L., Marsters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,
            South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Homo sapiens"
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                     /chromosome="1"
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                     /cell_type="endothelial"
                     /tissue_type="umbilical vein"
     gene            1. .534
                     /gene="TNFSF18"
     CDS             1. .534
                     /gene="TNFSF18"
                     /note="GITR ligand"
                     /codon_start=1
                     /product="glucocorticoid-induced TNFR-related protein
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                     /protein_id="AAD22634.1"
                     /db_xref="GI:4558501"
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                     IFIFLQLETAKEPCMAKFGPLPSKWQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVA
                     PNANYNDVAPFEVRLYKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLK
                     NNTYWGIILLANPQFIS"
ORIGIN

Alignment Scores:
Pred. No.:              2.58e-69        Length:         534
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AF125303 (1-534)

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Qy          21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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Qy          41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
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Qy          61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
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Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         442 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 501

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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RESULT 3
AR092586
LOCUS       AR092586                1849 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 1 from patent US 5998171.
ACCESSION   AR092586
VERSION     AR092586.1  GI:10019339
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Polynucleotides encoding human endokine alpha
  JOURNAL   Patent: US 5998171-A 1 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .1849
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ORIGIN

Alignment Scores:
Pred. No.:              1.11e-68        Length:         1849
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x AR092586 (1-1849)

Qy           1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Db         170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy          21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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Db         230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy          41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
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Db         290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy          61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
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Db         410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
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Db         470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
               ||||||||||||||||||||||||||||||
Db         530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 4
BD268764
LOCUS       BD268764                1849 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Human endokine alpha and methods of use.
ACCESSION   BD268764
VERSION     BD268764.1  GI:33078532
KEYWORDS    JP 2002537769-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.L., Ni,J. and Rosen,C.A.
  TITLE     Human endokine alpha and methods of use
  JOURNAL   Patent: JP 2002537769-A 1 12-NOV-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537769-A/1
            PD   12-NOV-2002
            PF   25-FEB-2000 JP 2000601183
            PR   26-FEB-1999 US    60/122099,28-MAY-1999 US    60/136788 PI
            GUO LIANG YU,JIAN NI,CRAIG A ROSEN
            PC   C12N15/09,A61K38/22,A61K39/395,A61K39/395,A61K45/00,A61P1/00,
            PC   A61P1/16,
            PC   A61P3/00,A61P3/08,A61P5/14,A61P7/06,A61P9/10,A61P11/06 PC
            ,A61P13/12,A61P17/02,
            PC   A61P17/06,A61P19/00,A61P19/02,A61P21/04,A61P25/00,A61P25/00,
            PC   A61P25/16,
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            PC   C07K16/24,
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            FH   Key             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.11e-68        Length:         1849
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1_COPY_48_177 (1-130) x BD268764 (1-1849)

Qy           1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
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Qy          21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy          41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349
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Qy          61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Db         350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
               |||||||||||||||||||||||||||||
Db         530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 5
AR214043
LOCUS       AR214043                1849 bp    mRNA    linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6406867.
ACCESSION   AR214043
VERSION     AR214043.1  GI:23311480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Antibody to human endokine alpha and methods of use
  JOURNAL   Patent: US 6406867-A 1 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1849
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ORIGIN

Alignment Scores:
Pred. No.:                1.11e-68       Length:          1849
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AR214043 (1-1849)

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Db         170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy          21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy          41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy          61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
               |||||||||||||||||||||||||||||
Db         530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 6
AR282586
LOCUS       AR282586                1849 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6521742.
ACCESSION   AR282586
VERSION     AR282586.1  GI:29719155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Human endokine alpha
  JOURNAL   Patent: US 6521742-A 1 18-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1849
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.11e-68       Length:          1849
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AR282586 (1-1849)

Qy           1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         170 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 229

Qy          21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         230 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 289

Qy          41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 349

Qy          61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 409

Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         410 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 469

Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         470 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATC 529

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
               |||||||||||||||||||||||||||||
Db         530 ATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 7
AX074393
LOCUS       AX074393                1964 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 13 from Patent WO0103720.
ACCESSION   AX074393
VERSION     AX074393.1  GI:12710533
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Williams,P.M. and Gerritsen,M.E.
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  TITLE     Promotion or inhibition of angiogenesis and cardiovascularization
            by tumor necrosis factor ligand/receptor homologs
  JOURNAL   Patent: WO 0103720-A 13 18-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-68       Length:          1964
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AX074393 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 8
AX077015
LOCUS       AX077015                1964 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 3 from Patent WO0105972.
ACCESSION   AX077015
VERSION     AX077015.1  GI:13121653
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0105972-A 3 25-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-68       Length:          1964
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AX077015 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              ||||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 9
AX080755
LOCUS       AX080755                1964 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 1 from Patent WO0109327.
ACCESSION   AX080755
VERSION     AX080755.1  GI:13169735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Method of preventing the injury or death of retinal cells and
            treating ocular diseases
  JOURNAL   Patent: WO 0109327-A 1 08-FEB-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-68       Length:          1964
Score:                    694.00         Matches:         130
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0
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US-09-195-368-1_COPY_48_177 (1-130) x AX080755 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
AX150805
LOCUS       AX150805                1964 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140464.
ACCESSION   AX150805
VERSION     AX150805.1  GI:14533039
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Ferrara,N., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Mark,M.R., Marsters,S.A., Paoni,N.F., Pitti,R.M. and
            Wood,W.I.
  TITLE     Interleukin-1-receptor associated kinase-3 (irak3) and its use in
            promotion or inhibition of angiogenesis and cardiovascularization
  JOURNAL   Patent: WO 0140464-A 1 07-JUN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-68      Length:          1964
Score:                    694.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       6             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AX150805 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 11
AX391258
LOCUS       AX391258                1964 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 1 from Patent WO0073445.
ACCESSION   AX391258
VERSION     AX391258.1  GI:19699932
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Williams,P.M., Baker,K.P., Ashkenazi,A.J., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Kuo,S.S., Mark,M.R., Marsters,S.A.,
            Pitti,R.M., Wood,W.I., Gerber,H., Gerritsen,M.E., Paoni,N.F. and
            Watanabe,C.K.
  TITLE     Promotion or inhibition of angiogenesis and cardiovascularization
  JOURNAL   Patent: WO 0073445-A 1 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-68      Length:          1964
Score:                    694.00        Matches:         130
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       6             Gaps:            0

US-09-195-368-1_COPY_48_177 (1-130) x AX391258 (1-1964)

Qy          1 PheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
              |||||||||||||||||||||||||||||
Db        522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551
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Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy         101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         462 ATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGTATC 521

Qy         121 IleLeuLeuAlaAsnProGlnPheIleSer 130
               |||||||||||||||||||||||||||||
Db         522 ATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 12
BD085993
LOCUS       BD085993                1964 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Tumor necrosis factor homolog DNA19355 polypeptide.
ACCESSION   BD085993
VERSION     BD085993.1  GI:22631603
KEYWORDS    JP 2001523459-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Robert, Pitti,
            Baker,K.P., Godowski,P.J. and Mark,M.R.
  TITLE     Tumor necrosis factor homolog DNA19355 polypeptide
  JOURNAL   Patent: JP 2001523459-A 1 27-NOV-2001;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001523459-A/1
            PD   27-NOV-2001
            PF   18-NOV-1998 JP 2000521199
            PR   18-NOV-1997 US    60/065635,12-DEC-1997 US    60/069661 PI
            AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT PI
            PITTI,KEVIN P BAKER,
            PI   PAUL J GODOWSKI,MELANIE R MARK
            PC   C12N15/09,A61K38/00,A61P35/00,C07K14/525,C07K16/24,C07K19/00,
            PC   C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02//C12P21/08,(C12P21/02,C12R1:19),
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            Location/Qualifiers
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ORIGIN

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Score:                  694.00         Matches:        130
Percent Similarity:     100.00%        Conservative:   0
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US-09-195-368-1_COPY_48_177 (1-130) x BD085993 (1-1964)

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Db         282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

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Db         342 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTA 401

Qy          81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
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DEFINITION  Novel tumor necrosis factor receptor homolog and nucleic acid
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VERSION     BD124038.1  GI:23218983
KEYWORDS    JP 2002502607-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            and Goddard,A.
  TITLE     Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same
  JOURNAL   Patent: JP 2002502607-A 14 29-JAN-2002;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502607-A/14
            PD   29-JAN-2002
            PF   09-FEB-1999 JP 2000530610
            PR   09-FEB-1998 US   60/074 087
            PI   AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT M
            PITTI,
            PI   WILLIAM I WOOD,AUDLEY GODDARD
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P29/00,A61P37/06,
            PC   A61P43/00,
            PC   C07K14/705,C07K16/28,C07K19/00,C12N1/19,C12N1/21,C12N5/10, PC
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            tumor necrosis factor receptor homolog and nucleic acid  CC
               encoding the
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-68       Length:         1964
Score:                  694.00         Matches:        130
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
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US-09-195-368-1_COPY_48_177 (1-130) x BD124038 (1-1964)
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Db        162 TTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCA 221

Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
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Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
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DEFINITION  Novel tumor necrosis factor receptor homolog and nucleic acid
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ACCESSION   BD124046
VERSION     BD124046.1  GI:23218991
KEYWORDS    JP 2002502607-A/22.
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            and Goddard,A.
  TITLE     Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same
  JOURNAL   Patent: JP 2002502607-A 22 29-JAN-2002;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502607-A/22
            PD   29-JAN-2002
            PF   09-FEB-1999 JP 2000530610
            PR   09-FEB-1998 US   60/074 087
            PI   AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT M
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            PI   WILLIAM I WOOD,AUDLEY GODDARD
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P29/00,A61P37/06,
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Pred. No.:                1.19e-68        Length:          1964
Score:                    694.00          Matches:         130
Percent Similarity:       100.00%         Conservative:    0
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US-09-195-368-1_COPY_48_177 (1-130) x BD124046 (1-1964)

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Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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ACCESSION   AY358868
VERSION     AY358868.1  GI:37182853
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
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            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
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            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
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  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-68        Length:         1964
Score:                  694.00          Matches:        130
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
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US-09-195-368-1_COPY_48_177 (1-130) x AY358868 (1-1964)

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Qy         21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
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Db        222 AAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTG 281

Qy         41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTAC 341

Qy         61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
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Qy         81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACC 461

Qy        101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIle 120
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Qy        121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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| c | 27 | 74.5 | 7.8 | 4027 | 1 | US-08-571-785-3 | Sequence 3, Appli |
| c | 28 | 74.5 | 7.8 | 4027 | 1 | US-08-571-785-4 | Sequence 4, Appli |
| c | 29 | 74.5 | 7.8 | 4027 | 4 | US-09-192-435-3 | Sequence 3, Appli |
| c | 30 | 74.5 | 7.8 | 4027 | 4 | US-09-192-435-4 | Sequence 4, Appli |
| c | 31 | 74.5 | 7.8 | 4027 | 4 | US-09-558-340-3 | Sequence 3, Appli |
| c | 32 | 74.5 | 7.8 | 4027 | 4 | US-09-558-340-4 | Sequence 4, Appli |
| | 33 | 74 | 7.8 | 935 | 6 | 5182196-3 | Patent No. 5182196 |
| | 34 | 74 | 7.8 | 1071 | 4 | US-09-205-815B-44 | Sequence 44, Appl |
| | 35 | 74 | 7.8 | 2339 | 4 | US-09-645-926A-6 | Sequence 6, Appli |
| | 36 | 74 | 7.8 | 2359 | 5 | PCT-US95-16980-1 | Sequence 1, Appli |
| | 37 | 74 | 7.8 | 2455 | 4 | US-09-167-109-3 | Sequence 3, Appli |
| c | 38 | 74 | 7.8 | 2925 | 4 | US-09-540-236-384 | Sequence 384, App |
| c | 39 | 74 | 7.8 | 99629 | 4 | US-09-596-002-37 | Sequence 37, Appl |
| c | 40 | 73.5 | 7.7 | 3814 | 4 | US-09-302-812-5 | Sequence 5, Appli |
| c | 41 | 73.5 | 7.7 | 3814 | 4 | US-09-511-477-5 | Sequence 5, Appli |
| c | 42 | 73.5 | 7.7 | 3814 | 4 | US-09-511-507-5 | Sequence 5, Appli |
| c | 43 | 73 | 7.7 | 1305 | 4 | US-09-252-991A-7171 | Sequence 7171, Ap |
| | 44 | 73 | 7.7 | 2079 | 4 | US-09-252-991A-7332 | Sequence 7332, Ap |
| | 45 | 73 | 7.7 | 2124 | 4 | US-09-252-991A-7474 | Sequence 7474, Ap |

ALIGNMENTS

RESULT 1
US-08-912-227-1
; Sequence 1, Application US/08912227
; Patent No. 5998171
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,227
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,058
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-08-912-227-1

Alignment Scores:
Pred. No.:                6.54e-118       Length:          1849
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       2               Gaps:            0

US-09-195-368-1 (1-177) x US-08-912-227-1 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 2
US-09-513-584-1
; Sequence 1, Application US/09513584
; Patent No. 6406867
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  Human Endokine Alpha and Methods
;    TITLE OF INVENTION:  of Use
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX,
;      ADDRESSEE:  P.L.L.C
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/513,584
;      FILING DATE:  25-FEB-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/024,058
;      FILING DATE:  16-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/912,227
;      FILING DATE:  15-AUG-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/122,099
;      FILING DATE:  26-FEB-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/136,788
;      FILING DATE:  28-MAY-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/345,790
;      FILING DATE:  01-JUL-1999
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0470005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-09-513-584-1

Alignment Scores:
Pred. No.:                6.54e-118       Length:          1849
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       4               Gaps:            0

US-09-195-368-1 (1-177) x US-09-513-584-1 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268
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Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
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Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559
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RESULT 3
US-09-345-790-1
; Sequence 1, Application US/09345790
; Patent No. 6521742
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,790
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..559
US-09-345-790-1

Alignment Scores:

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| Pred. No.: | 6.54e-118 | Length: | 1849 |
| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-195-368-1 (1-177) x US-09-345-790-1 (1-1849)

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Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
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Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559
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RESULT 4
US-09-620-312D-30
; Sequence 30, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105

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;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 30
;   LENGTH: 3650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (319)..(1452)
US-09-620-312D-30

Alignment Scores:
Pred. No.:              1.12          Length:        3650
Score:                  85.50         Matches:       32
Percent Similarity:     40.91%        Conservative:  31
Best Local Similarity:  20.78%        Mismatches:    54
Query Match:            8.99%         Indels:        37
DB:                     4             Gaps:          6

US-09-195-368-1 (1-177) x US-09-620-312D-30 (1-3650)

Qy          26 LeuTrpLeuPheCysSerIleValMet------LeuLeuPheLeuCysSerPheSerTrp 43
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Db         697 ATTTGGTTTGGATGCAAACTAGTCCTGAACCCATCAGCAATAAACATCAACTTCAACCTC 756

Qy          44 LeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGly 63
               ::::::   :::   |||:::|||       |||             :::|||
Db         757 ATCCTGCTGCTCCTGCTGGAGCTGCTCATGGCGGCCACGGTGATCATCGCT--------- 807

Qy          64 ProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSer 83
                                   |||||||||       |||       |||
Db         808 --------------------GCACGGTCCAGCGAGGAGGACTGCAAGAAAAAG------ 840

Qy          84 AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaPro 103
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Db         841 ------------------------------------------AAGGGCTCCATGTCTGAC 858

Qy         104 AsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMet 123
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Db         859 AGCGCCAACATTCTGGACGAAGTGCCATTTCCTGCTCGGGTCCTGAAATCTTACTCAGTC 918

Qy         124 IleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHis 143
               ::::::   :::          |||   :::      :::||||||          |||:::
Db         919 GTCGAGGTAATCGCAGGCATCTCTGCCGTC------CTCGGGGGGATCATTGCCCTGAAC 972

Qy         144 ValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 163
               |||   |||::::::             :::      |||       :::         |||
Db         973 GTGGATGACTCAGTT------------TCAGGCCCACACCTCTCAGTG---------ACG 1011

Qy         164 TyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
               ::::::  |||::::::          |||       |||:::
Db        1012 TTCTTTTGGATCCTAGTGGCCTGCTTTCCAAGTGCCATTGCC 1053

RESULT 5
US-09-354-138-130
; Sequence 130, Application US/09354138
; Patent No. 6309647
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Taylor, Jill
;    APPLICANT:  Gettig, Russell
;    TITLE OF INVENTION:  POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
;    TITLE OF INVENTION:  RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
;    TITLE OF INVENTION:  RECOMBINANTS
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue, 25th Floor
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/354,138
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,379
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/416,646
;      FILING DATE:  05-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/224,657
;      FILING DATE:  16-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,962
;      FILING DATE:  08-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/776,867
;      FILING DATE:  23-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/621,614
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,283
;      FILING DATE:  31-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/105,483
;      FILING DATE:  12-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/847,951
;      FILING DATE:  06-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/713,967
;      FILING DATE:  11-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07,666,056
;      FILING DATE:  07-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2860
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1008 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-354-138-130

Alignment Scores:
Pred. No.:              0.186         Length:        1008
Score:                  84.50         Matches:       35
Percent Similarity:     45.16%        Conservative:  21
Best Local Similarity:  28.23%        Mismatches:    38
Query Match:            8.89%         Indels:        30
DB:                     4             Gaps:          8

US-09-195-368-1 (1-177) x US-09-354-138-130 (1-1008)

Qy          39 CysSerPheSer---Trp--------------LeuIlePheIlePheLeuGlnLeuGlu 52
               |||   ||||||   |||                  ::::::          ||||||||||||
Db         152 TGTATATTTTCTTAATGGGTATAATAGAAGACAATGATGGCCTCGGACCTCCAATTGGAA 211

Qy          53 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 72
                        :::   |||:::   :::   |||   |||             :::
Db         212 GAACATTTGGATCGCTGCCTTTAGGAGTTGGGCGTACTACAGCCAGACCTGAGGAGTTAT 271
```

```
Qy          73 SerSerGluProProCysValAsnLysValSerAspTrp---------------LysLeu 87
               :::|||||||||                  |||                 :::|||
Db         272 TGAAAGAAGCCACCCTGT-----------------TGGATATTATGGTAAGGCGAACTG 313

Qy          88 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsn-AlaAsnTy 107
               ::::::   :::|||       |||   |||         :::   |||::: |||:::
Db         314 CAGGTGTCAAGGAACAACTGGTATTTTATA---------ATAACACCCCATTGCACATCT 364

Qy         107 rAsnAspVal------AlaProPheGluValArgLeuTyrLysAsnLysAspMetIle-- 124
               |||   |||        |||:::|||   :::       :::   |||      :::
Db         365 TAACTCCGTGGAAAAAGGTCCTTACGAGTGGAAGTGTGTTCAGTGCAAATCAAGTCTGTA 424

Qy         125 ------------GlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTy 140
                          |||:::   :::   :::||||||||||      ||||||   ||
Db         425 ACACAGTCAATCTAATACCATTAGACATAGCACAAAGATTCAG------GGTGGTATATA 478

Qy         140 rGluLeuHis 143
               ||||   |||
Db         479 TGAGCATCAC 488
```

RESULT 6
US-09-107-532A-305
; Sequence 305, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3666 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...3666
; SEQUENCE DESCRIPTION: SEQ ID NO: 305:
US-09-107-532A-305

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.53 | Length: | 3666 |
| Score: | 84.50 | Matches: | 19 |
| Percent Similarity: | 57.58% | Conservative: | 19 |
| Best Local Similarity: | 28.79% | Mismatches: | 23 |
| Query Match: | 8.89% | Indels: | 5 |
| DB: | 4 | Gaps: | 1 |

US-09-195-368-1 (1-177) x US-09-107-532A-305 (1-3666)

```
Qy         102 AlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 121
               |||||||||              |||   :::   |||   :::   :::   :::|||:::
Db        1543 GCTCCTAATGGCTACCAACTAGATTCAAGCGAATTTTCAATTACAGTTAAAGAAAATCAA 1602

Qy         122 AspMetIleGlnThrLeuThrAsnLysSer--------------LysIleGlnAsnVal 136
               ::::::    |||   |||||||||                  :::|||:::   :::
Db        1603 AATGTTACTACCACAAGAACCAATAAGAAATCCACAGGTTCTGTAGAAATTGAAAAGATA 1662

Qy         137 GlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHis 156
               |||          |||   :::   :::   :::      |||:::||||||::::::
Db        1663 GGCGATTTAGATGGATTAGGACTACCGAATGTAGTATTCACGATTTATAATTCCGATAAC 1722

Qy         157 GlnValLeuLysAsnAsn 162
               :::|||:::|||:::|||
Db        1723 AAAGTTGTAAAAGATAAC 1740
```

RESULT 7
US-09-621-976-13182
; Sequence 13182, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13182
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13182

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 0.095 | Length: | 457 |
| Score: | 82.50 | Matches: | 41 |
| Percent Similarity: | 37.57% | Conservative: | 24 |
| Best Local Similarity: | 23.70% | Mismatches: | 45 |
| Query Match: | 8.68% | Indels: | 63 |
| DB: | 4 | Gaps: | 9 |

US-09-195-368-1 (1-177) x US-09-621-976-13182 (1-457)

```
Qy           6 LeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTrpLys 25
               |||   :::   |||   |||   |||     :::   ||||||       |||||||||
Db          23 CTCCCGCACCGCCCGGYSTCCCCATCTGCCTGGCGTTGTGCGCAG------AGCTGGAAA 76

Qy          26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIle 45
                                                                :::||||||:::
Db          77 ----------------------------------------------GCATGGCTGTTG 88

Qy          46 PheIlePheLeuGlnLeuGluThrAlaLysGluProCys---------------------- 58
               :::::|||||||:::                |||||
Db          89 TATGTATTCTTGCGC-----------------CCGTGTGACAACATTTAAACTTCTAAA 130

Qy          59 --------------MetAlaLysPheGlyProLeuProSerLys-------------- 68
                           :::                |||   |||
Db         131 AACGGAACCTCCTTCCGTGTTAGGATTGCAAGTTAACCTAGGAAAAACAGCATTCTGCAA 190
```

```
Qy          69 ---------TrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrp 85
Db         191 ATTATTTGCTGGAAAATCTCGGTGACTTAAGGCCCATGTATTACT--------------- 235

Qy          86 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyr-Gly---GlnValAlaProAs 104
Db         236 ------------TTGCAGGGGTCTCTCACTCTAGTTTACTGGTGTAGATTTTTTAAAAAA 283

Qy         104 nAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIl 124
Db         284 TCCATCTTATCAAAAAATA---CCGTTTAAGGTGGAAAATTTCAAATGCAAGTCGCAGTT 340

Qy         124 eGlnThrLeuThr------------------Asn-LysSerLysIleGlnAsnValGlyG 138
Db         341 GATGAGATTGCAATTAATATATTTDAGATAGAATTAGAGAAAAACTACAGTCAGTGCATA 400

Qy         138 lyThrTyrGluLeuHisValGlyAspThrIleAsp 149
Db         401 TTAAGTATTTTTTTCATATTTTGGGGGGATTAGAT 435

RESULT 8
US-09-851-985-3/c
; Sequence 3, Application US/09851985
; Patent No. 6670150
; GENERAL INFORMATION:
;  APPLICANT: GONG, Fangcheng et al.
;  TITLE OF INVENTION: ISOLATED HUMAN RECEPTOR PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN RECEPTOR PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001238
;  CURRENT APPLICATION NUMBER: US/09/851,985
;  CURRENT FILING DATE:  2001-05-10
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 21968
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(21968)
;   OTHER INFORMATION: n = A,T,C or G
US-09-851-985-3

Alignment Scores:
Pred. No.:                99.1          Length:          21968
Score:                    80.50         Matches:         29
Percent Similarity:       45.45%        Conservative:    11
Best Local Similarity:    32.95%        Mismatches:      27
Query Match:              8.46%         Indels:          21
DB:                       4             Gaps:            5

US-09-195-368-1 (1-177) x US-09-851-985-3 (1-21968)

Qy           4 SerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSer 23
Db       17227 TCTCACAGAGAGAACCTGAACGGGACAGGGTTGAGGGAGCAGGGGCCCCAGAGAAGGACA 17168

Qy          24 TrpLysLeu--------------TrpLeuPheCysSerIleVal---------MetLeu 35
Db       17167 TGGGACATGGATTCAGTCTTTCCGTGGCTCAGGAGCTCCATCCTCCATGCTGAGCTCAAG 17108

Qy          36 LeuPheLeuCys--------------SerPheSerTrpLeuIlePheIlePheLeuGln 50
Db       17107 GTCTTCCTCTGCAAGGCTGGTACCCTCTCCCTTTTGACCTTAAAGTCCATCCTCCTTCAG 17048

Qy          51 LeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGln 70
Db       17047 CACCAGGCTCATGCCCAGCCT------GTGCACTGGGCAACCCTTCCATCATTCTATCAA 16994

Qy          71 MetAlaSerSerGluProProCys 78
Db       16993 -----------------CCATGC 16988
```

```
RESULT 9
US-09-230-380-10
; Sequence 10, Application US/09230380A
; Patent No. 6172215
; GENERAL INFORMATION:
;  APPLICANT: Keshi, Hiroyuki
;  APPLICANT: Eda, Soji
;  APPLICANT: Uehara, Hirotsugu
;  APPLICANT: Nishida, Keigo
;  APPLICANT: Matsuhisa, Akio
;  TITLE OF INVENTION: Probes For Detecting and Identifying Helicobacter
;  TITLE OF INVENTION: Pylori
;  FILE REFERENCE: 19036/35268
;  CURRENT APPLICATION NUMBER: US/09/230,380A
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1219
;   TYPE: DNA
;   ORGANISM: Helicobacter pylori
US-09-230-380-10

Alignment Scores:
Pred. No.:                1.03          Length:          1219
Score:                    80.00         Matches:         37
Percent Similarity:       37.57%        Conservative:    28
Best Local Similarity:    21.39%        Mismatches:      58
Query Match:              8.41%         Indels:          50
DB:                       3             Gaps:            8

US-09-195-368-1 (1-177) x US-09-230-380-10 (1-1219)

Qy          13 HisSerArgThrGlnGlyAlaGlnArgSerSerTrpLysLeuTrpLeuPheCysSerIle 32
Db         361 CATTTAAAAGGCAAGGTCATGAATAGTTCTAATCTCAAAAATTGGCTGTTCCCTACCATT 420

Qy          33 ValMetLeuLeuPheLeuCysSerPheSerTrpLeuIlePheIlePheLeuGln------ 50
Db         421 TGCTTTTTTTTGTTTTGTTATATTTTAATTTTTTTGATGTTTTTTATGTTTAAAAGTTTG 480

Qy          51 ----------------------LeuGluThrAlaLysGluProCysMetAla------ 60
Db         481 CAATCGCAATCTTTTGGCTCTGTGGCAGAAACCGGAAAAAAACCCATCACCACCACCAAG 540

Qy          61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
Db         541 AAATTTGGTAAGGAATTGCAAAAACAG--------------------------ATTTCA 573

Qy          81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
Db         574 AAGATC--------------------------CATTAACTTTTTTTCTTTTTTGCCGAT 606

Qy         101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
Db         607 ACTTGCCGTAATGGA--------------------ATGAATATCAAATTA---AAGGAT 642

Qy         121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
Db         643 TTTACAATGATCAATGCCGTTTCTTCTCTTTCTCCGGTGCAATCTGTGGGGAATTACAAG 702

Qy         141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlu--------------- 155
Db         703 CGTGTGGAAAAGAATGAAAAAGTTGAA---------AATAGCGAGGCCGCTCTTGATAGG 753

Qy         156 ------------HisGlnValLeuLysAsnAsnThrTyr 164
Db         754 GTGGCTGAAATCAAGCAAGCTATTGAAAACAACCAGTAT 792

RESULT 10
US-09-078-294-13/c
; Sequence 13, Application US/09078294
```

```
; Patent No. 6265211
; GENERAL INFORMATION:
;  APPLICANT: Choo, Kong-Hong Andy
;  APPLICANT: Du Sart, Desiree
;  APPLICANT: Cancilla, Michael R.
;  TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
;  FILE REFERENCE: Davies Col
;  CURRENT APPLICATION NUMBER: US/09/078,294
;  CURRENT FILING DATE: 1998-05-13
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 7505
;   TYPE: DNA
;   ORGANISM: BAC-F2 contig 9
US-09-078-294-13

Alignment Scores:
Pred. No.:                27.3          Length:          7505
Score:                    79.00         Matches:         32
Percent Similarity:       39.68%        Conservative:    18
Best Local Similarity:    25.40%        Mismatches:      26
Query Match:              8.31%         Indels:          50
DB:                       3             Gaps:            7

US-09-195-368-1 (1-177) x US-09-078-294-13 (1-7505)

Qy         14 SerArgThrGlnGlyAlaGlnArgSerSerTrp-----------LysLeuTrp------ 27
              |||:::|||   |||   ::::::||||||           |||   |||
Db       6143 TCTCAAACTCCTGGCCTCAAGCAGTCCTCCCACCCTGGCCTCCCAAAGTGTTGGGCTTAC 6084

Qy         28 -------------------------------------------LeuPheCysSerIle 32
                                                         :::|||      :::
Db       6083 AGGCATGAGCCACCGTGCCCGGCCCTGTTAAGCCTTTCTATCTAGATTTTTTCCCTCCTA 6024

Qy         33 ValMetLeuLeuPheLeuCysSerPheSerTrpLeuIlePheIlePheLeuGlnLeuGlu 52
              :::||||||:::|||   |||   ||||||::|||            |||:::
Db       6023 ATCATGTTGGTGTTTTTTTGTTTGTTTTCATTTTTGTTTTGTTTTGTTTTGAGACGGAGT 5964

Qy         53 ThrAlaLysGluProCysMetAlaLysPheGly------------------------- 63
                 |||           :::|||:::   |||
Db       5963 TTTGCT---------CTTGTTGCCCAAGCTGGTGTGCAATGGCACGATCTCGGTTCACCG 5913

Qy         64 ---ProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 82
                 ||||||||||||:::::::::      |||           |||::::::
Db       5912 CAACCTCTGCCTTCCAGGTTCAAACGATTCTCC-----------TGCCTCAGCCCCCAG 5865

Qy         83 SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAla 102
              |||   |||                                  |||       |||
Db       5864 AGTAGCTGGGAT-------------------------------TACAGGCATGTGCCA 5838

Qy        103 ProAsn---AlaAsnTyr 107
              |||:::   ||||||:::
Db       5837 CCACACCTGGCTAATTTT 5820

RESULT 11
US-08-845-998-7/c
; Sequence 7, Application US/08845998
; Patent No. 5879892
;  GENERAL INFORMATION:
;    APPLICANT:  Van Baren, Nicolas
;    APPLICANT:  Coulie, Pierre G.
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  Boon, Thierry
;    TITLE OF INVENTION:  LEUKEMIA ASSOCIATED GENES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/845,998
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)720-3500
;      TELEFAX:  (617)720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4524 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  174..1433
US-08-845-998-7

Alignment Scores:
Pred. No.:                16.3          Length:          4524
Score:                    78.00         Matches:         19
Percent Similarity:       47.54%        Conservative:    10
Best Local Similarity:    31.15%        Mismatches:      24
Query Match:              8.20%         Indels:          8
DB:                       2             Gaps:            1

US-09-195-368-1 (1-177) x US-08-845-998-7 (1-4524)

Qy         26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIle 45
              |||   |||||||||   :::::::::   |||:::|||   ||||||   ||||||:::
Db       1924 TTGCTTTTGTTCTGTTTTGTTTTAGTTTGTCTTTATTTGTCTAGTTTTTGGTGGTTGGTA 1865

Qy         46 PheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLys------------ 61
                 :::||||||   :::                        :::   |||
Db       1864 GGTTTGTTTTTGTACATAGTTCCTTGGTCCCCAGGATATTTAGGTAAGTGTCTCTGGTCA 1805

Qy         62 ------------PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProPro 77
                         |||       ||||||:::                  :::   ||||||
Db       1804 GAAACAGTCCATTTTCCTACCCTTCCCGCGTCTCCCCCCACCCAAACCCCAGAACCATCC 1745

Qy         78 Cys 78
              |||
Db       1744 TGC 1742

RESULT 12
US-09-206-537-7/c
; Sequence 7, Application US/09206537
; Patent No. 6130052
;  GENERAL INFORMATION:
;    APPLICANT:  Van Baren, Nicolas
;    APPLICANT:  Coulie, Pierre G.
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  Boon, Thierry
;    TITLE OF INVENTION:  LEUKEMIA ASSOCIATED GENES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
```

```
;       STATE:  MA
;       COUNTRY:  US
;       ZIP:  02210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/206,537
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/845,998
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER:  40,212
;       REFERENCE/DOCKET NUMBER:  L0461/7008
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)720-3500
;       TELEFAX:  (617)720-2441
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4524 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  174..1433
US-09-206-537-7

Alignment Scores:
Pred. No.:                16.3          Length:          4524
Score:                    78.00         Matches:         19
Percent Similarity:       47.54%        Conservative:    10
Best Local Similarity:    31.15%        Mismatches:      24
Query Match:              8.20%         Indels:          8
DB:                       3             Gaps:            1

US-09-195-368-1 (1-177) x US-09-206-537-7 (1-4524)

Qy         26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIle 45
              |||   |||||||||   :::::::::   |||:::|||   ||||||   ||||||:::
Db       1924 TTGCTTTTGTTCTGTTTTGTTTTAGTTTGTCTTTATTTGTCTAGTTTTTGGTGGTTGGTA 1865

Qy         46 PheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLys------------ 61
                :::||||||   :::                 :::   |||
Db       1864 GGTTTGTTTTTGTACATAGTTCCTTGGTCCCCAGGATATTTAGGTAAGTGTCTCTGGTCA 1805

Qy         62 ------------PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProPro 77
                        |||      ||||||:::             :::   ||||||
Db       1804 GAAACAGTCCATTTTCCTACCCTTCCCGCGTCTCCCCCCACCCAAACCCCAGAACCATCC 1745

Qy         78 Cys 78
              |||
Db       1744 TGC 1742

RESULT 13
US-09-430-854-7/c
; Sequence 7, Application US/09430854
; Patent No. 6271019
;  GENERAL INFORMATION:
;     APPLICANT:  Van Baren, Nicolas
;     APPLICANT:  Coulie, Pierre G.
;     APPLICANT:  De Smet, Charles
;     APPLICANT:  Lucas, Sophie
;     APPLICANT:  Boon, Thierry
;     TITLE OF INVENTION:  LEUKEMIA ASSOCIATED GENES
;     NUMBER OF SEQUENCES:  16
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;       STREET:  600 Atlantic Avenue
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  US
;       ZIP:  02210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/430,854
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/845,998
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER:  40,212
;       REFERENCE/DOCKET NUMBER:  L0461/7008
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)720-3500
;       TELEFAX:  (617)720-2441
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4524 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  174..1433
US-09-430-854-7

Alignment Scores:
Pred. No.:                16.3          Length:          4524
Score:                    78.00         Matches:         19
Percent Similarity:       47.54%        Conservative:    10
Best Local Similarity:    31.15%        Mismatches:      24
Query Match:              8.20%         Indels:          8
DB:                       3             Gaps:            1

US-09-195-368-1 (1-177) x US-09-430-854-7 (1-4524)

Qy         26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIle 45
              |||   |||||||||   :::::::::   |||:::|||   ||||||   ||||||:::
Db       1924 TTGCTTTTGTTCTGTTTTGTTTTAGTTTGTCTTTATTTGTCTAGTTTTTGGTGGTTGGTA 1865

Qy         46 PheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLys------------ 61
                :::||||||   :::                 :::   |||
Db       1864 GGTTTGTTTTTGTACATAGTTCCTTGGTCCCCAGGATATTTAGGTAAGTGTCTCTGGTCA 1805

Qy         62 ------------PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProPro 77
                        |||      ||||||:::             :::   ||||||
Db       1804 GAAACAGTCCATTTTCCTACCCTTCCCGCGTCTCCCCCCACCCAAACCCCAGAACCATCC 1745

Qy         78 Cys 78
              |||
Db       1744 TGC 1742

RESULT 14
5395759-1
;Patent No. 5395759
;     APPLICANT: HOLMES, IAN H.;DYALL-SMITH, MICHAEL L.
;     TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE
;ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN
```

```
;    NUMBER OF SEQUENCES: 14
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/474,642
;      FILING DATE: 29-APR-1985
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 824,704
;      FILING DATE: 04-FEB-1987
;SEQ ID NO:1:
;      LENGTH: 1062
5395759-1

Alignment Scores:
Pred. No.:              2.08          Length:        1062
Score:                  77.00         Matches:       42
Percent Similarity:     38.59%        Conservative:  29
Best Local Similarity:  22.83%        Mismatches:    59
Query Match:            8.10%         Indels:        54
DB:                     6             Gaps:          9

US-09-195-368-1 (1-177) x 5395759-1 (1-1062)

Qy         26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCys----------Ser 40
Db         76 CTGACCATTTTGATATCTATCATATTATTGAATTATATATTAAAAACTATAACTAATACG 135

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
Db        136 ATGGACTACATAATTTTCAGGTTTTTACTACTCATTGCTTTAATATCACCATTTGTAAGG 195

Qy         61 Lys--------------------------PheGlyProLeuProSerLysTrpGlnMet 71
Db        196 ACACAAAATTATGGCATGTATTTACCAATAACGGGATCACTAGACGCTGTATATACGAAT 255

Qy         72 AlaSerSerGluProPro----------CysVal---------- 79
Db        256 TCTACTAGTGGAGAGCCATTTTTAACTTCGACGCTGTGTTTATACTATCCAGCAGAAGCT 315

Qy         80 ---AsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyr 98
Db        316 AAAAATGAGATTTCAGATGATGAATGGGAAAATACTTTATCACAATTATTTTTAACTAAA 375

Qy         99 GlyGlnValAlaProAsnAla---------AsnTyrAsnAspValAlaProPheGluVal 115
Db        376 GGATGGCCAATTGGATCAGTTTATTTTAAAGACTACAATGATATTAATACATTTTCTGTG 435

Qy        116 ------ArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIle 133
Db        436 AATCCACAACTATATTGTGATTATAATGTAGTA----------TTG 471

Qy        134 GlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsn 153
Db        472 ATGAGATATGACAATACATCTGAATTAGATGCATCAGAGTTAGCAGATCTTATATTGAAT 531

Qy        154 SerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnPro 173
Db        532 GAA----------TGG----------CTGTGCAATCCT 549

Qy        174 GlnPheIleSer 177
Db        550 ATGGATATATCG 561

RESULT 15
US-09-976-594-668/c
; Sequence 668, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 668
;   LENGTH: 4446
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 001322.4
US-09-976-594-668

Alignment Scores:
Pred. No.:              21.6          Length:        4446
Score:                  77.00         Matches:       37
Percent Similarity:     35.56%        Conservative:  11
Best Local Similarity:  27.41%        Mismatches:    35
Query Match:            8.10%         Indels:        52
DB:                     4             Gaps:          8

US-09-195-368-1 (1-177) x US-09-976-594-668 (1-4446)

Qy          3 LeuSerHis---LeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArg 21
Db        422 TTAAGCCACTCTTCTTCCAATTCTCCCTCATCAGGCTCTTTGACAACAACCACCTCTTGA 363

Qy         22 SerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer--- 40
Db        362 TCTTCT---------TGGCTGTTT---TCACTAGATTTCTTGATGTTTTCTAGTTCTATC 315

Qy         40 ------------------------------------------------------------ 40
Db        314 CAATAGTCTTCCATAGATAGTTCATCCAAAGAATCCTGGGAAATTGATCGATCAAATGGA 255

Qy         41 --------------------------PheSerTrpLeuIle------PheIlePheLeu 49
Db        254 GGCTTCTCCATAACTTTGATGGTGGTGCTTTCCTGGTTCATAGTGTACTGGCCATATCTG 195

Qy         50 GlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyPro----------Leu 65
Db        194 CGACTCGAGGTGGCTTCCTCCCCTGCCTTTGCATGGCTGTTCCCGACGGCCTGGTCCTTG 135

Qy         66 ProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrp 85
Db        134 CCGCTGGGGTGGTAGGCTGTTAGTACCACTCCC----------TGG 99

Qy         86 LysLeuGlu---------IleLeuGlnAsnGlyLeuTyrLeuIle 97
Db         98 GAACTGGAGAGCCAGCTCATGGTGAGAGAAGGGACATACTTTCTG 54

Search completed: April  7, 2004, 21:12:08
Job time : 87.0684 secs
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GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:55:16 ; Search time 2642.89 Seconds
(without alignments)
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Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENMPLSHSRTQGAQ.....VLKNNTYWGIILLANPQFIS 177

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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33: em_htg_mus:*
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35: em_htg_rod:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 951 | 100.0 | 534 | 9 | AF125303 | AF125303 Homo sapi |
| 2 | | 951 | 100.0 | 1849 | 6 | AR092586 | AR092586 Sequence |
| 3 | | 951 | 100.0 | 1849 | 6 | BD268764 | BD268764 Human end |
| 4 | | 951 | 100.0 | 1849 | 6 | AR214043 | AR214043 Sequence |
| 5 | | 951 | 100.0 | 1849 | 6 | AR282586 | AR282586 Sequence |
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| 7 | | 951 | 100.0 | 1964 | 6 | AX077015 | AX077015 Sequence |
| 8 | | 951 | 100.0 | 1964 | 6 | AX080755 | AX080755 Sequence |
| 9 | | 951 | 100.0 | 1964 | 6 | AX150805 | AX150805 Sequence |
| 10 | | 951 | 100.0 | 1964 | 6 | AX391258 | AX391258 Sequence |
| 11 | | 951 | 100.0 | 1964 | 6 | BD085993 | BD085993 Tumor nec |
| 12 | | 951 | 100.0 | 1964 | 6 | BD124038 | BD124038 Novel tum |
| 13 | c | 951 | 100.0 | 1964 | 6 | BD124046 | BD124046 Novel tum |
| 14 | | 951 | 100.0 | 1964 | 9 | AY358868 | AY358868 Homo sapi |
| 15 | | 906 | 95.3 | 510 | 9 | AF117713 | AF117713 Homo sapi |
| 16 | | 628 | 66.0 | 163136 | 9 | HS15D23 | AL031599 Human DNA |
| 17 | | 419.5 | 44.1 | 568 | 10 | AY234223 | AY234223 Mus muscu |
| 18 | | 419.5 | 44.1 | 1261 | 10 | MMU577580 | AJ577580 Mus muscu |
| 19 | | 419.5 | 44.1 | 2066 | 10 | MMU577579 | AJ577579 Mus muscu |
| 20 | | 414.5 | 43.6 | 522 | 10 | AY267900 | AY267900 Mus muscu |
| 21 | | 413.5 | 43.5 | 528 | 10 | AY320040 | AY320040 Mus muscu |
| 22 | | 412.5 | 43.4 | 522 | 10 | AY359852 | AY359852 Mus muscu |
| 23 | | 333.5 | 35.1 | 228107 | 2 | AC109057 | AC109057 Rattus no |
| 24 | | 317.5 | 33.4 | 116159 | 2 | AC117819 | AC117819 Mus muscu |
| 25 | | 108.5 | 11.4 | 892 | 5 | GGA243435 | AJ243435 Gallus ga |
| 26 | c | 106.5 | 11.2 | 248545 | 2 | AC112050 | AC112050 Rattus no |
| 27 | c | 106.5 | 11.2 | 283198 | 2 | AC131215 | AC131215 Rattus no |
| 28 | c | 103.5 | 10.9 | 178980 | 10 | AL669897 | AL669897 Mouse DNA |
| 29 | c | 99.5 | 10.5 | 182737 | 10 | AL772354 | AL772354 Mouse DNA |
| 30 | c | 98.5 | 10.4 | 78616 | 10 | AC000398 | AC000398 Genomic s |
| 31 | c | 98 | 10.3 | 140287 | 9 | HSDJ407E4 | AL121949 Human DNA |
| 32 | | 98 | 10.3 | 253059 | 2 | AC095984 | AC095984 Rattus no |
| 33 | c | 98 | 10.3 | 254829 | 2 | AC103318 | AC103318 Rattus no |
| 34 | c | 97.5 | 10.3 | 165501 | 2 | AC037468 | AC037468 Homo sapi |
| 35 | c | 97.5 | 10.3 | 169063 | 9 | AC098677 | AC098677 Homo sapi |
| 36 | c | 97.5 | 10.3 | 171403 | 9 | AC092701 | AC092701 Homo sapi |
| 37 | c | 97.5 | 10.3 | 173041 | 2 | AC069320 | AC069320 Homo sapi |
| 38 | c | 97.5 | 10.3 | 179222 | 2 | AC090270 | AC090270 Homo sapi |
| 39 | c | 97 | 10.2 | 153096 | 2 | AC022044 | AC022044 Homo sapi |
| 40 | c | 97 | 10.2 | 153295 | 2 | AC060758 | AC060758 Homo sapi |
| 41 | | 97 | 10.2 | 189219 | 9 | AC020595 | AC020595 Homo sapi |
| 42 | | 95.5 | 10.0 | 67793 | 2 | AC016116 | AC016116 Homo sapi |
| 43 | | 95.5 | 10.0 | 124949 | 9 | AL358794 | AL358794 Human DNA |
| 44 | c | 95.5 | 10.0 | 300050 | 9 | AB100084 | AB100084 Pan trogl |
| 45 | | 95 | 10.0 | 166032 | 2 | AC023645 | AC023645 Homo sapi |

ALIGNMENTS

RESULT 1

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LOCUS       AF125303                534 bp    mRNA    linear   PRI 02-APR-1999
DEFINITION  Homo sapiens glucocorticoid-induced TNFR-related protein ligand
            (TNFSF18) mRNA, complete cds.
ACCESSION   AF125303
VERSION     AF125303.1  GI:4558500
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Gurney,A.L., Marsters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
  TITLE     Identification of a new member of the tumor necrosis factor family
            and its receptor, a human ortholog of mouse GITR
  JOURNAL   Curr. Biol. (1999) In press
REFERENCE   2  (bases 1 to 534)
  AUTHORS   Gurney,A.L., Marsters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,
            South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .534
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                     /mol_type="mRNA"
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                     /translation="MCLSHLENMPLSHSRTQGAQRSSWKLWLFCSIVMLLFLCSFSWL
                     IFIFLQLETAKEPCMAKFGPLPSKWQMASSEPPCVNKVSDWKLEILQNGLYLIYGQVA
                     PNANYNDVAPFEVRLYKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLK
                     NNTYWGIILLANPQFIS"
ORIGIN

Alignment Scores:
Pred. No.:                3.63e-97        Length:          534
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-195-368-1 (1-177) x AF125303 (1-534)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
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Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 2
AR092586
LOCUS       AR092586                1849 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 1 from patent US 5998171.
ACCESSION   AR092586
VERSION     AR092586.1  GI:10019339
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Polynucleotides encoding human endokine alpha
  JOURNAL   Patent: US 5998171-A 1 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .1849
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.78e-96        Length:          1849
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-195-368-1 (1-177) x AR092586 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328
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Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 3
BD268764
LOCUS       BD268764                1849 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Human endokine alpha and methods of use.
ACCESSION   BD268764
VERSION     BD268764.1  GI:33078532
KEYWORDS    JP 2002537769-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.L., Ni,J. and Rosen,C.A.
  TITLE     Human endokine alpha and methods of use
  JOURNAL   Patent: JP 2002537769-A 1 12-NOV-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537769-A/1
            PD   12-NOV-2002
            PF   25-FEB-2000 JP 2000601183
            PR   26-FEB-1999 US    60/122099,28-MAY-1999 US    60/136788 PI
            GUO LIANG YU,JIAN NI,CRAIG A ROSEN
            PC   C12N15/09,A61K38/22,A61K39/395,A61K39/395,A61K45/00,A61P1/00,
            PC   A61P1/16,
            PC   A61P3/00,A61P3/08,A61P5/14,A61P7/06,A61P9/10,A61P11/06 PC
            ,A61P13/12,A61P17/02,
            PC   A61P17/06,A61P19/00,A61P19/02,A61P21/04,A61P25/00,A61P25/00,
            PC   A61P25/16,
            PC   A61P25/28,A61P27/02,A61P29/00,A61P31/04,A61P33/00,A61P35/00,
            PC   A61P35/02,
            PC   A61P37/02,A61P37/04,A61P37/06,A61P37/08,A61P43/00,C07K14/52,
            PC   C07K16/24,
            PC   C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/
            PC   00,A61K37/24
            CC   endokine alpha protein
            FH   Key             Location/Qualifiers
            FT   CDS             (53)...(559).
FEATURES              Location/Qualifiers
     source           1. .1849
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:                1.78e-96        Length:         1849
Score:                    951.00          Matches:        177
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-09-195-368-1 (1-177) x BD268764 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 4
AR214043
LOCUS       AR214043                1849 bp    mRNA    linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6406867.
ACCESSION   AR214043
VERSION     AR214043.1  GI:23311480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Antibody to human endokine alpha and methods of use
  JOURNAL   Patent: US 6406867-A 1 18-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .1849
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.78e-96        Length:         1849
Score:                    951.00          Matches:        177
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       6               Gaps:           0

US-09-195-368-1 (1-177) x AR214043 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208
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Qy          61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy          81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy         101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy         121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy         141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy         161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 5
AR282586
LOCUS       AR282586                1849 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6521742.
ACCESSION   AR282586
VERSION     AR282586.1  GI:29719155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1849)
  AUTHORS   Yu,G.-L., Ni,J. and Rosen,C.A.
  TITLE     Human endokine alpha
  JOURNAL   Patent: US 6521742-A 1 18-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1849
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.78e-96        Length:         1849
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1 (1-177) x AR282586 (1-1849)

Qy           1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy          21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy          41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy          61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy          81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy         101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy         121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy         141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy         161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 6
AX074393
LOCUS       AX074393                1964 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 13 from Patent WO0103720.
ACCESSION   AX074393
VERSION     AX074393.1  GI:12710533
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Williams,P.M. and Gerritsen,M.E.
  TITLE     Promotion or inhibition of angiogenesis and cardiovascularization
            by tumor necrosis factor ligand/receptor homologs
  JOURNAL   Patent: WO 0103720-A 13 18-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.93e-96        Length:         1964
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1 (1-177) x AX074393 (1-1964)

Qy           1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy          21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy          41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy          61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy          81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy         101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
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Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140

Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160

Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177

Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 7
AX077015
LOCUS       AX077015               1964 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 3 from Patent WO0105972.
ACCESSION   AX077015
VERSION     AX077015.1  GI:13121653
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0105972-A 3 25-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                 1.93e-96        Length:          1964
Score:                     951.00          Matches:         177
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               100.00%         Indels:          0
DB:                        6               Gaps:            0

US-09-195-368-1 (1-177) x AX077015 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20

Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40

Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60

Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80

Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100

Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120

Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140

Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160

Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177

Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 8
AX080755
LOCUS       AX080755               1964 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 1 from Patent WO0109327.
ACCESSION   AX080755
VERSION     AX080755.1  GI:13169735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Method of preventing the injury or death of retinal cells and
            treating ocular diseases
  JOURNAL   Patent: WO 0109327-A 1 08-FEB-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                 1.93e-96        Length:          1964
Score:                     951.00          Matches:         177
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               100.00%         Indels:          0
DB:                        6               Gaps:            0

US-09-195-368-1 (1-177) x AX080755 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20

Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40

Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60

Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80

Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100

Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120

Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380
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Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 9
AX150805
LOCUS       AX150805               1964 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140464.
ACCESSION   AX150805
VERSION     AX150805.1  GI:14533039
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Ferrara,N., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Mark,M.R., Marsters,S.A., Paoni,N.F., Pitti,R.M. and
            Wood,W.I.
  TITLE     Interleukin-1-receptor associated kinase-3 (irak3) and its use in
            promotion or inhibition of angiogenesis and cardiovascularization
  JOURNAL   Patent: WO 0140464-A 1 07-JUN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.93e-96        Length:          1964
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-195-368-1 (1-177) x AX150805 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
AX391258
LOCUS       AX391258               1964 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 1 from Patent WO0073445.
ACCESSION   AX391258
VERSION     AX391258.1  GI:19699932
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Williams,P.M., Baker,K.P., Ashkenazi,A.J., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Kuo,S.S., Mark,M.R., Marsters,S.A.,
            Pitti,R.M., Wood,W.I., Gerber,H., Gerritsen,M.E., Paoni,N.F. and
            Watanabe,C.K.
  TITLE     Promotion or inhibition of angiogenesis and cardiovascularization
  JOURNAL   Patent: WO 0073445-A 1 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.93e-96        Length:          1964
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-195-368-1 (1-177) x AX391258 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 11
BD085993
LOCUS       BD085993                1964 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Tumor necrosis factor homolog DNA19355 polypeptide.
ACCESSION   BD085993
VERSION     BD085993.1  GI:22631603
KEYWORDS    JP 2001523459-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Robert, Pitti,
            Baker,K.P., Godowski,P.J. and Mark,M.R.
  TITLE     Tumor necrosis factor homolog DNA19355 polypeptide
  JOURNAL   Patent: JP 2001523459-A 1 27-NOV-2001;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001523459-A/1
            PD   27-NOV-2001
            PF   18-NOV-1998 JP 2000521199
            PR   18-NOV-1997 US    60/065635,12-DEC-1997 US    60/069661 PI
            AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT PI
            PITTI,KEVIN P BAKER,
            PI   PAUL J GODOWSKI,MELANIE R MARK
            PC   C12N15/09,A61K38/00,A61P35/00,C07K14/525,C07K16/24,C07K19/00,
            PC   C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02//C12P21/08,(C12P21/02,C12R1:19),
            PC   (C12P21/02,C12R1:91),C12N15/00,A61K37/02,C12N5/00 CC   Tumor
            necrosis factor homolog DNA19355 polypeptide FH   Key
            Location/Qualifiers
            FT   source          1. .1964
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.93e-96        Length:         1964
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1 (1-177) x BD085993 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 12
BD124038
LOCUS       BD124038                1964 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same.
ACCESSION   BD124038
VERSION     BD124038.1  GI:23218983
KEYWORDS    JP 2002502607-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            and Goddard,A.
  TITLE     Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same
  JOURNAL   Patent: JP 2002502607-A 14 29-JAN-2002;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502607-A/14
            PD   29-JAN-2002
            PF   09-FEB-1999 JP 2000530610
            PR   09-FEB-1998 US   60/074 087
            PI   AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT M
            PITTI,
            PI   WILLIAM I WOOD,AUDLEY GODDARD
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P29/00,A61P37/06,
            PC   A61P43/00,
            PC   C07K14/705,C07K16/28,C07K19/00,C12N1/19,C12N1/21,C12N5/10, PC
             C12P21/02,
            PC   C12Q1/68//C07K14/47,C12N15/00,A61K37/02,C12N5/00 CC   Novel
            tumor necrosis factor receptor homolog and nucleic acid  CC
               encoding the
            CC   same
            FH   Key             Location/Qualifiers
            FT   source          1. .1964
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1964
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.93e-96        Length:         1964
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
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Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-09-195-368-1 (1-177) x BD124038 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
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Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 13
BD124046/c
LOCUS       BD124046                1964 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same.
ACCESSION   BD124046
VERSION     BD124046.1  GI:23218991
KEYWORDS    JP 2002502607-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            and Goddard,A.
  TITLE     Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same
  JOURNAL   Patent: JP 2002502607-A 22 29-JAN-2002;
            GENENTECH INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502607-A/22
            PD   29-JAN-2002
            PF   09-FEB-1999 JP 2000530610
            PR   09-FEB-1998 US   60/074 087
            PI   AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT M
            PITTI,
            PI   WILLIAM I WOOD,AUDLEY GODDARD
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P29/00,A61P37/06,
            PC   A61P43/00,
            PC   C07K14/705,C07K16/28,C07K19/00,C12N1/19,C12N1/21,C12N5/10, PC
             C12P21/02,
            PC   C12Q1/68//C07K14/47,C12N15/00,A61K37/02,C12N5/00 CC   Novel
            tumor necrosis factor receptor homolog and nucleic acid  CC
               encoding the
            CC   same
            FH   Key             Location/Qualifiers
            FT   source          1. .1964
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .1964
                      ./organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.93e-96        Length:         1964
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-195-368-1 (1-177) x BD124046 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db       1944 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 1885

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
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Db       1884 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 1825

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 1765

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 1705

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
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Db       1704 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 1645

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 1585

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 1525

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 1465

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 1414

RESULT 14
AY358868
LOCUS       AY358868                1964 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA19355 GITRL (UNQ149) mRNA, complete cds.
ACCESSION   AY358868
VERSION     AY358868.1  GI:37182853
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1964)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
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            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
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            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1964)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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     CDS             21. .554
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ORIGIN

Alignment Scores:
Pred. No.:                1.93e-96        Length:          1964
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-195-368-1 (1-177) x AY358868 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
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Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
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Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
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Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 15
AF117713
LOCUS       AF117713                 510 bp    mRNA    linear   PRI 09-MAR-1999
DEFINITION  Homo sapiens AITR ligand (TL6) mRNA, complete cds.
ACCESSION   AF117713
VERSION     AF117713.1  GI:4378801
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Kwon,B., Yu,K.Y., Ni,J., Yu,G.L., Jang,I.K., Kim,Y.J., Xing,L.,
            Liu,D., Wang,S.X. and Kwon,B.S.
  TITLE     Identification of a novel activation-inducible protein of the tumor
            necrosis factor receptor superfamily and its ligand
  JOURNAL   J. Biol. Chem. 274 (10), 6056-6061 (1999)
  MEDLINE   99156876
   PUBMED   10037686
REFERENCE   2  (bases 1 to 510)
  AUTHORS   Kwon,B., Yu,K.Y., Ni,J. and Kwon,B.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-1999) Micro. & Immunol., Indiana University, 635
            Barnhill Dr., Indianapolis, IN 46202, USA
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     gene            1. .510
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                     LLANPQFIS"
ORIGIN

Alignment Scores:
Pred. No.:                3.77e-92        Length:          510
Score:                    906.00          Matches:         169
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              95.27%          Indels:          0
DB:                       9               Gaps:            0

US-09-195-368-1 (1-177) x AF117713 (1-510)

Qy          9 MetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTrpLysLeuTrpLeu 28
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAGAGATCATCCTGGAAGCTGTGGCTC 60

Qy         29 PheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIlePheIlePhe 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCCTTCAGTTGGCTAATCTTTATTTTT 120
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Qy          49 LeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLys 68
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCTAAGTTTGGACCATTACCCTCAAAA 180

Qy          69 TrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeuGlu 88
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAG 240

Qy          89 IleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyrAsn 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATACTTCAGAATGGCTTATATTTAATTTATGGCCAAGTGGCTCCCAATGCAAACTACAAT 300

Qy         109 AspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThr 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAACAAAGACATGATACAAACTCTAACA 360

Qy         129 AsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIle 148
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Db         361 AACAAATCTAAAATCCAAAATGTAGGAGGGACTTATGAATTGCATGTTGGGGACACCATA 420

Qy         149 AspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyIleIle 168
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Db         421 GACTTGATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACCTACTGGGGTATCATT 480

Qy         169 LeuLeuAlaAsnProGlnPheIleSer 177
               |||||||||||||||||||||||||
Db         481 TTACTGGCAAATCCCCAATTCATCTCC 507
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Search completed: April 7, 2004, 18:25:29
Job time : 2661.89 secs

GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 16:50:59 ; Search time 2423.23 Seconds
(without alignments)
2181.225 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENMPLSHSRTQGAQ.....VLKNNTYWGIILLANPQFIS 177

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061638_2606/app_query.fasta_1.654
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09195368_@CGN_1_1_5436_@runat_07042004_061638_2606 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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27: em_gss_vrl:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 951 | 100.0 | 634 | 13 | BX473859 | BX473859 DKFZp686K |
| 2 | 608 | 63.9 | 669 | 29 | AG182677 | AG182677 Pan trogl |
| 3 | 294 | 30.9 | 350 | 13 | BY216375 | BY216375 BY216375 |
| 4 | 240 | 25.2 | 348 | 13 | BY214208 | BY214208 BY214208 |
| 5 | 209.5 | 22.0 | 334 | 13 | BY326400 | BY326400 BY326400 |
| 6 | 198.5 | 20.9 | 328 | 13 | BY326606 | BY326606 BY326606 |
| 7 | 194.5 | 20.5 | 324 | 13 | BY327839 | BY327839 BY327839 |
| 8 | 192.5 | 20.2 | 672 | 29 | AG043514 | AG043514 Pan trogl |
| c 9 | 117 | 12.3 | 114 | 29 | CG977950 | CG977950 CH240_168 |
| 10 | 110 | 11.6 | 727 | 13 | BU294618 | BU294618 603603621 |
| 11 | 110 | 11.6 | 731 | 13 | BU373331 | BU373331 603589056 |
| 12 | 96 | 10.1 | 1514 | 28 | CC250868 | CC250868 CH261-17B |
| 13 | 95.5 | 10.0 | 842 | 13 | BX709408 | BX709408 BX709408 |
| 14 | 93 | 9.8 | 808 | 29 | CC508168 | CC508168 CH240_350 |
| 15 | 91.5 | 9.6 | 506 | 13 | BU996000 | BU996000 HM12B02r |
| 16 | 90.5 | 9.5 | 788 | 14 | CK000102 | CK000102 AGENCOURT |
| 17 | 90.5 | 9.5 | 922 | 13 | BX355834 | BX355834 BX355834 |
| 18 | 90.5 | 9.5 | 985 | 12 | BM460288 | BM460288 AGENCOURT |
| 19 | 90.5 | 9.5 | 1024 | 12 | BM919028 | BM919028 AGENCOURT |
| 20 | 90 | 9.5 | 611 | 13 | BQ869292 | BQ869292 QGD5L18.y |
| 21 | 90 | 9.5 | 932 | 10 | BE536333 | BE536333 601062531 |
| 22 | 89.5 | 9.4 | 600 | 14 | CD127418 | CD127418 MF1-0016G |
| c 23 | 89.5 | 9.4 | 673 | 13 | BU345361 | BU345361 604171455 |
| c 24 | 89.5 | 9.4 | 823 | 14 | CF831057 | CF831057 UCRCR01_0 |
| 25 | 88.5 | 9.3 | 563 | 10 | BF490152 | BF490152 AT26450_5 |
| 26 | 88.5 | 9.3 | 632 | 14 | CA263424 | CA263424 SCRLLB203 |
| 27 | 88.5 | 9.3 | 686 | 14 | CA179879 | CA179879 SCCCST200 |
| c 28 | 88.5 | 9.3 | 747 | 29 | AG029081 | AG029081 Pan trogl |
| 29 | 88.5 | 9.3 | 943 | 13 | BQ891935 | BQ891935 AGENCOURT |
| 30 | 88 | 9.3 | 638 | 9 | AI982044 | AI982044 pat.pk007 |
| 31 | 88 | 9.3 | 644 | 29 | CE207073 | CE207073 tigr-gss- |
| c 32 | 88 | 9.3 | 701 | 28 | AZ870214 | AZ870214 2M0182C10 |
| 33 | 88 | 9.3 | 840 | 29 | CG058482 | CG058482 PUFTI80TD |
| c 34 | 88 | 9.3 | 850 | 14 | CF289682 | CF289682 AGENCOURT |
| 35 | 87.5 | 9.2 | 469 | 12 | BG658667 | BG658667 TgESTzya3 |
| 36 | 87.5 | 9.2 | 714 | 29 | CC955012 | CC955012 BOIEJ81TR |
| 37 | 87.5 | 9.2 | 855 | 13 | BX843917 | BX843917 BX843917 |
| 38 | 87 | 9.1 | 617 | 28 | AQ471661 | AQ471661 CITBI-E1- |
| 39 | 87 | 9.1 | 635 | 29 | CE798899 | CE798899 tigr-gss- |
| c 40 | 87 | 9.1 | 789 | 12 | BM049470 | BM049470 603623401 |
| c 41 | 87 | 9.1 | 1096 | 12 | BG398113 | BG398113 602440150 |
| 42 | 86.5 | 9.1 | 515 | 28 | AQ477698 | AQ477698 CITBI-E1- |
| 43 | 86.5 | 9.1 | 656 | 28 | AZ869907 | AZ869907 2M0182O07 |
| 44 | 86.5 | 9.1 | 750 | 28 | BZ597628 | BZ597628 WHAAQ30TR |
| c 45 | 86 | 9.0 | 696 | 13 | BQ858845 | BQ858845 QGC11G11. |

ALIGNMENTS

RESULT 1
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LOCUS BX473859 634 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686K13165_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686K13165 5', mRNA sequence.
ACCESSION BX473859
VERSION BX473859.1 GI:31668103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 634)

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  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686K13165) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
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Query Match:            100.00%         Indels:         0
DB:                     13              Gaps:           0

US-09-195-368-1 (1-177) x BX473859 (1-634)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
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Db        105 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 164

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 224

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 464

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 524

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        525 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 575

RESULT 2
AG182677
LOCUS       AG182677                669 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-055O22.T7, genomic survey
            sequence.
ACCESSION   AG182677
VERSION     AG182677.1  GI:16712357
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                Sequencing: T7
             LIBRARY
                Vector    : pBACe3.6
                R.Site 1  : EcoRI
                R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-055O22.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN

Alignment Scores:
Pred. No.:              2.8e-62         Length:         669
Score:                  608.00          Matches:        114
Percent Similarity:     95.04%          Conservative:   1
Best Local Similarity:  94.21%          Mismatches:     6
Query Match:            63.93%          Indels:         0
DB:                     29              Gaps:           0

US-09-195-368-1 (1-177) x AG182677 (1-669)

Qy         57 ProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluPro 76
              ||||||:::          ||||||||||||||||||||||||||||||||||||||||
Db        258 CCTTGTATATTTCTTACAGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCT 317

Qy         77 ProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeu 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTA 377

Qy         97 IleTyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArg 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATTTATGGCCAAGTGGCTCCCAATGCAAACTACAATGATGTAGTTCCTTTTGAGGTGCGG 437

Qy        117 LeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnVal 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CTGTATAAAAACAAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTA 497
```

```
Qy        137 GlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHis 156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GGAGGGACTTATGAATTGCATGTTGGGGACACCATAGACTAGATATTTAACTCTGAGCAT 557

Qy        157 GlnValLeuLysAsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIle 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        558 CAGGTTCTAAAAAATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAACTTATT 617

Qy        177 Ser 177
              |||
Db        618 TCC 620
```

RESULT 3
BY216375
LOCUS BY216375 350 bp mRNA linear EST 10-DEC-2002
DEFINITION BY216375 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830044F01 5', mRNA sequence.
ACCESSION BY216375
VERSION BY216375.1 GI:26397123
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 350)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .350
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830044F01"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 5.92e-25 | Length: | 350 |
| Score: | 294.00 | Matches: | 62 |
| Percent Similarity: | 65.49% | Conservative: | 12 |
| Best Local Similarity: | 54.87% | Mismatches: | 37 |
| Query Match: | 30.91% | Indels: | 2 |
| DB: | 13 | Gaps: | 2 |

US-09-195-368-1 (1-177) x BY216375 (1-350)

```
Qy         53 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 72
              ||||||  |||  ||||||  ||||||                ||||||||  |||
Db         10 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 69

Qy         73 SerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsn 92
              |||   :::|||   |||||||||      ||||||  ||||||:::|||||||||:::
Db         70 TCTCCCAAACCTCACTGTGTGAATACGACATCTGATGGGAAGCTGAAGATACTGCAGAGT 129

Qy         93 GlyLeuTyrLeuIleTyrGlyGlnValAlaPro---AsnAlaAsnTyr---AsnAspVal 110
              |||   ||||||||||||||||||||   |||   :::      |||      |||
Db        130 GGCACATATTTAATCTACGGCCAAGTGATTCCTGTGGATAAGAAATACATAAAAGACAAT 189

Qy        111 AlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLys 130
              |||||||||   |||:::::::||||||      |||:::::|||||||||   |||
Db        190 GCCCCCTTCGTAGTACAGATATATAAAAAGAATGATGTCCTACAAACTCTAATGAATGAT 249

Qy        131 SerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeu 150
                 :::|||      :::||||||  ||||||||||||  ||||||  |||  |||
Db        250 TTTCAAATCTTGCCTATAGGAGGGGTTTATGAACTGCATGCTGGAGATAACATATATCTG 309

Qy        151 IlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 163
                 |||||||||:::      :::  |||  ||||||
Db        310 AAGTTCAACTCTAAAGACCATATTCAGAAAACTAACACA 348
```

RESULT 4
BY214208
LOCUS BY214208 348 bp mRNA linear EST 10-DEC-2002
DEFINITION BY214208 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830027N19 5', mRNA sequence.
ACCESSION BY214208

VERSION BY214208.1 GI:26394920
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .348
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830027N19"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.82e-18 | Length: | 348 |
| Score: | 240.00 | Matches: | 60 |
| Percent Similarity: | 62.28% | Conservative: | 11 |
| Best Local Similarity: | 52.63% | Mismatches: | 40 |
| Query Match: | 25.24% | Indels: | 4 |
| DB: | 13 | Gaps: | 2 |

US-09-195-368-1 (1-177) x BY214208 (1-348)

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Qy         53 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 72
              ||||||   |||   ||||||  ||||||              |||||||||   |||
Db         10 ACTGCCATCGAGTCCTGCATGGTTAAGTTTGAACTATCATCCTCAAAATGGCACATGACA 69

Qy         73 SerSerGluProProCysValAsnLysValSerAsp-TrpLysLeuGluIleLeuGlnAs 92
                 |||:::        ||||||       ||||||    ||||||:::|||||||||::
Db         70 TC-TCCCAAACTCAATGGGTGAATACGACATCTGATGGGGAAGCTGAAGATACTGCAGAG 128

Qy         92 nGlyLeuTyrLeuIleTyrGlyGlnValAlaPro---AsnAlaAsnTyr---AsnAspVa 110
              :|||   ||||||||||||||||||||   |||   :::      |||     |||
Db        129 TGGCACATATTTAATCTACGGCCAAGTGATTCCTGTGGATAAGAAATACATAAAAGACAA 188

Qy        110 lAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLy 130
              |||||||||   |||::::::||||||      |||::::::|||||||||   |||
Db        189 GGCCCCCTTCGTAGTACAGATATATAAAAAGAATGATGTCCTACAAACTCTAATGAATGA 248

Qy        130 sSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLe 150
                :::|||      :::||||||   ||||||||||||   ||||||   |||   ||
Db        249 TTTTCAAATCTTGCCTATAGGAGGGGTTTATGAACTGCATGCTGGAGATAACATATATCT 308

Qy        150 uIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 163
              |   |||||||||:::            |||   ||||||
Db        309 GAAGTTCAACTCTAAAGACCATANTCAGAAAACTAACACA 348
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RESULT 5
BY326400
LOCUS BY326400 334 bp mRNA linear EST 11-DEC-2002
DEFINITION BY326400 RIKEN full-length enriched, synovial fibroblasts Mus musculus cDNA clone L030036A22 5', mRNA sequence.
ACCESSION BY326400
VERSION BY326400.1 GI:26516959
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 334)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .334
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030036A22"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 7.95e-15 | Length: | 334 |
| Score: | 209.50 | Matches: | 49 |
| Percent Similarity: | 60.42% | Conservative: | 9 |
| Best Local Similarity: | 51.04% | Mismatches: | 35 |
| Query Match: | 22.03% | Indels: | 3 |
| DB: | 13 | Gaps: | 3 |

US-09-195-368-1 (1-177) x BY326400 (1-334)

```
Qy          4 SerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSer 23
              |||   :::|||   |||||||||      |||      |||   |||:::|||
Db         51 AGCCTCATGGAGGAAATGCCTTTGAGAGAATCAAGTCCTCAAAGGGCAGAGAGGTGCAAG 110

Qy         24 TrpLysLeuTrpLeuPheCysSerIleValMetLeuLeu---PheLeuCysSerPheSer 42
                |||   ||||||   |||   :::   :::||||||      |||||||||
Db        111 ---AAGTCATGGCTCTTGTGCATAGTGGCTCTGTTACTGATGTTGCTCTGTTCTTTGGGT 167

Qy         43 TrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPhe 62
                ||||||:::      |||:::      ||||||   |||   ||||||   ||||||
Db        168 ACACTGATCTATACTTCACTCAAG---CCAACTGCCATCGAGTCCTGCATGGTTAAGTTT 224

Qy         63 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 82
                         |||||||||   |||   |||   :::|||   |||||||||
Db        225 GAACTATCATCCTCAAAATGGCACATGACATCTCCCAAACCTCACTGTGTGAATACGACA 284

Qy         83 SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyr 98
              ||||||   ||||||:::|||||||||:::|||   ||||||||||||
Db        285 TCTGATGGGAAGCTGAAGATACTGCAGAGTGGCACATATTTAATCTAC 332
```

RESULT 6
BY326606
LOCUS BY326606 328 bp mRNA linear EST 11-DEC-2002
DEFINITION BY326606 RIKEN full-length enriched, synovial fibroblasts Mus musculus cDNA clone L030037A06 5', mRNA sequence.
ACCESSION BY326606
VERSION BY326606.1 GI:26517167
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 328)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .328
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030037A06"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.63e-13 | Length: | 328 |
| Score: | 198.50 | Matches: | 47 |
| Percent Similarity: | 59.57% | Conservative: | 9 |
| Best Local Similarity: | 50.00% | Mismatches: | 35 |
| Query Match: | 20.87% | Indels: | 3 |
| DB: | 13 | Gaps: | 3 |

US-09-195-368-1 (1-177) x BY326606 (1-328)

```
Qy          4 SerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSer 23
              |||   :::|||   |||||||||      |||      |||   |||:::|||
Db         51 AGCCTCATGGAGGAAATGCCTTTGAGAGAATCAAGTCCTCAAAGGGCAGAGAGGTGCAAG 110

Qy         24 TrpLysLeuTrpLeuPheCysSerIleValMetLeuLeu---PheLeuCysSerPheSer 42
                 |||   ||||||   |||   :::   :::||||||      |||||||||
Db        111 ---AAGTCATGGCTCTTGTGCATAGTGGCTCTGTTACTGATGTTGCTCTGTTCTTTGGGT 167

Qy         43 TrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPhe 62
              ||||||:::      |||:::      ||||||   |||   ||||||   ||||||
Db        168 ACACTGATCTATACTTCACTCAAG---CCAACTGCCATCGAGTCCTGCATGGTTAAGTTT 224

Qy         63 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 82
                    |||||||||   |||   |||   :::|||   |||||||||
Db        225 GAACTATCATCCTCAAAATGGCACATGACATCTCCCAAACCTCACTGTGTGAATACGACA 284

Qy         83 SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeu 96
              ||||||   ||||||:::||||||||||:::|||   ||||||
```

Db 285 TCTGATGGGAAGCTGAAGATACTGCAGAGTGGCACATATTTA 326

RESULT 7
BY327839
LOCUS BY327839 324 bp mRNA linear EST 11-DEC-2002
DEFINITION BY327839 RIKEN full-length enriched, synovial fibroblasts Mus musculus cDNA clone L030044D24 5', mRNA sequence.
ACCESSION BY327839
VERSION BY327839.1 GI:26518410
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="L030044D24"
                     /cell_type="synovial fibroblasts"
                     /clone_lib="RIKEN full-length enriched, synovial
                     fibroblasts"
ORIGIN
```

Alignment Scores:

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| Pred. No.: | 4.83e-13 | Length: | 324 |
| Score: | 194.50 | Matches: | 46 |
| Percent Similarity: | 59.14% | Conservative: | 9 |
| Best Local Similarity: | 49.46% | Mismatches: | 35 |
| Query Match: | 20.45% | Indels: | 3 |
| DB: | 13 | Gaps: | 3 |

US-09-195-368-1 (1-177) x BY327839 (1-324)

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Qy          4 SerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSer 23
              |||   :::|||   |||||||||     |||     |||   |||:::|||
Db         51 AGCCTCATGGAGGAAATGCCTTTGAGAGAATCAAGTCCTCAAAGGGCAGAGAGGTGCAAG 110

Qy         24 TrpLysLeuTrpLeuPheCysSerIleValMetLeuLeu---PheLeuCysSerPheSer 42
                |||   ||||||   |||   :::   :::||||||      |||||||||
Db        111 ---AAGTCATGGCTCTTGTGCATAGTGGCTCTGTTACTGATGTTGCTCTGTTCTTTGGGT 167

Qy         43 TrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPhe 62
                ||||||:::      |||:::      ||||||   |||   ||||||   ||||||
Db        168 ACACTGATCTATACTTCACTCAAG---CCAACTGCCATCGAGTCCTGCATGGTTAAGTTT 224

Qy         63 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 82
                      |||||||||   |||   |||   :::|||   |||||||||
Db        225 GAACTATCATCCTCAAAATGGCACATGACATCTCCCAAACCTCACTGTGTGAATACGACA 284

Qy         83 SerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyr 95
              ||||||   ||||||:::|||||||||:::|||   |||
Db        285 TCTGATGGGAAGCTGAAGATACTGCAGAGTGGCACATAT 323
```

```
RESULT 8
AG043514
LOCUS       AG043514                672 bp    DNA     linear   GSS 01-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-021N15.R, genomic survey sequence.
ACCESSION   AG043514
VERSION     AG043514.1  GI:16572239
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 672)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                Sequencing: M13Rev
             LIBRARY
                Vector    : pKS145
                R.Site 1  : SacI
                R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-021N15.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
```

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.54e-12 | Length: | 672 |
| Score: | 192.50 | Matches: | 38 |
| Percent Similarity: | 87.23% | Conservative: | 3 |
| Best Local Similarity: | 80.85% | Mismatches: | 3 |
| Query Match: | 20.24% | Indels: | 3 |
| DB: | 29 | Gaps: | 1 |

US-09-195-368-1 (1-177) x AG043514 (1-672)

```
Qy         10 ProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTrpLysLeuTrpLeuPhe 29
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Db         44 CCGCTAGCATGCTCGAGA---------GCTCAGAGATCATCCTGGAAGCTGTGGCTCTTT 94

Qy         30 CysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIlePheIlePheLeu 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 TGCTCAATAGTTATGTTGCTATTTCTTTGCTCCTTCAGTTGGCTAATCTTTATTTTTCTC 154

Qy         50 GlnLeuGluThrAlaLysGlu 56
              |||||||||       ::::::
Db        155 CAATTAGAGGTAAGGAGGCAA 175
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RESULT 9
CG977950/c
LOCUS       CG977950                114 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  CH240_168J10.TV CHORI-240 Bos taurus genomic clone CH240_168J10,
            genomic survey sequence.
ACCESSION   CG977950
VERSION     CG977950.1  GI:39903729
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 114)
  AUTHORS   Costa,J.N., Mota,M. and Caetano,A.R.
  TITLE     Brazil's Contribution to End-Sequencing the Bovine BAC Library
            CHORI-240
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: CH240_168J10.TJ
            Contact: Caetano AR
            Department of Biotechnology
            Embrapa Recursos Geneticos e Biotecnologia
            Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
            02372, 70770-900 Brasil
            Tel: 55 61 448 4778
            Fax: 55 61 340 3658
            Email: acaetano@cenargen.embrapa.br
```

Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher then 20. Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm).
This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 168 row: J column: 10
Seq primer: T7
Class: BAC ends
High quality sequence stop: 114.

FEATURES Location/Qualifiers
source 1. .114
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_168J10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 0.000206 | Length: | 114 |
| Score: | 117.00 | Matches: | 19 |
| Percent Similarity: | 85.19% | Conservative: | 4 |
| Best Local Similarity: | 70.37% | Mismatches: | 4 |
| Query Match: | 12.30% | Indels: | 0 |
| DB: | 29 | Gaps: | 0 |

US-09-195-368-1 (1-177) x CG977950 (1-114)

```
Qy          63 GlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysVal 82
               ||||||||||||||||||||||||||||   |||   ||||||   |||:::||||||
Db          81 GGACCATTACCTTCAAAATGGCAAATGCCTTCTCCTGAGCCTTCTTGTATGAATAAGACA 22

Qy          83 SerAspTrpLysLeuGluIle 89
               :::||||||:::|||:::|||
Db          21 GCTGACTGGAGGCTGAAGATA 1
```

RESULT 10
BU294618
LOCUS BU294618 727 bp mRNA linear EST 27-NOV-2002
DEFINITION 603603621F1 CSEQCHN55 Gallus gallus cDNA clone ChEST582i6 5', mRNA sequence.
ACCESSION BU294618
VERSION BU294618.1 GI:25744254
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 727)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES Location/Qualifiers
source 1. .727
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 15I"
/db_xref="taxon:9031"
/clone="ChEST582i6"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN55"
/note="Organ: kidney + adrenal; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

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|---|---|---|---|
| Pred. No.: | 0.0238 | Length: | 727 |
| Score: | 110.00 | Matches: | 38 |
| Percent Similarity: | 48.03% | Conservative: | 23 |
| Best Local Similarity: | 29.92% | Mismatches: | 46 |
| Query Match: | 11.57% | Indels: | 20 |
| DB: | 13 | Gaps: | 6 |

US-09-195-368-1 (1-177) x BU294618 (1-727)

```
Qy          62 PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLys 81
               |||  |||:::     ||||||  |||   :::|||    |||     :::
Db         184 TTCTCCCCAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCCAACGAGCAGCTTG 237

Qy          82 ValSer------AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 99
               :::|||     :::   ||||||::::::   :::   |||||||||   ||||||
Db         238 ATATCCTACCATGAGGGGAAGCTGAAGGTGGAGAAAGCAGGGCTCTACTACATCTACTCA 297

Qy         100 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr--- 118
               ||||||:::                 |||||||||   :::   :::|||
Db         298 CAAGTCAGCTTCTGCACCAAGGCGGCGGCTTCGGCGCCATTCACCCTCTATATTTATTTG 357

Qy         119 --------------------------------LysAsnLysAspMetIleGlnThrLeu 127
                                               |||     |||         |||
Db         358 TACCTCCCCATGGAAGAGGACCGGCTCCTGATGAAGGGACTTGACACGCACAGCACCTCC 417

Qy         128 ThrAsnLysSerLysIleGlnAsnVal------GlyGlyThrTyrGluLeuHisValGly 145
               |||         ::::::|||::::::      ||||||   :::||||||       |||
Db         418 ACGGCTCTCTGTGAGCTCCAGTCCATCCGGGAGGGCGGTGTCTTCGAGCTGCGGCAGGGC 477

Qy         146 AspThr------IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 163
               |||         :::::::::     ::::::        |||         ||||||
Db         478 GACATGGTCTTTGTCAATGTGACGGACTCAACAGCAGTGAACGTCAACCCTGGCAACACC 537

Qy         164 TyrTrpGlyIleIleLeuLeu 170
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Db         538 TACTTTGGCATGTTCAAGCTG 558
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RESULT 11
BU373331
LOCUS BU373331 731 bp mRNA linear EST 28-NOV-2002
DEFINITION 603589056F1 CSEQCHN74 Gallus gallus cDNA clone ChEST549p13 5', mRNA

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            sequence.
ACCESSION   BU373331
VERSION     BU373331.1  GI:25881332
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST549p13"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN74"
                     /note="Organ: kidney + adrenal; Vector: pBluescript II
                     KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
                     library was constructed from 1 million independent clones.
                     cDNA synthesis was initiated using an oligo(dT) primer,
                     using methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN

Alignment Scores:
Pred. No.:                0.024          Length:          731
Score:                    110.00         Matches:         38
Percent Similarity:       48.03%         Conservative:    23
Best Local Similarity:    29.92%         Mismatches:      46
Query Match:              11.57%         Indels:          20
DB:                       13             Gaps:            6

US-09-195-368-1 (1-177) x BU373331 (1-731)

Qy          62 PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLys 81
               |||   |||:::     ||||||   |||   :::|||       |||          :::
Db         186 TTCTCCCCAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCCAACGAGCAGCTTG 239

Qy          82 ValSer------AspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly 99
               :::|||      :::   ||||||::::::   :::   |||||||||   ||||||
Db         240 ATATCCTACCATGAGGGGAAGCTGAAGGTGGAGAAAGCAGGGCTCTACTACATCTACTCA 299

Qy         100 GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyr--- 118
               ||||||:::                          |||||||||   :::   :::|||
Db         300 CAAGTCAGCTTCTGCACCAAGGCGGCGGCTTCGGCGCCATTCACCCTCTATATTTATTTG 359

Qy         119 --------------------------------LysAsnLysAspMetIleGlnThrLeu 127
                                               |||         |||         |||
Db         360 TACCTCCCCATGGAAGAGGACCGGCTCCTGATGAAGGGACTTGACACGCACAGCACCTCC 419

Qy         128 ThrAsnLysSerLysIleGlnAsnVal------GlyGlyThrTyrGluLeuHisValGly 145
               |||         ::::::|||::::::      ||||||   :::|||||||      |||
Db         420 ACGGCTCTCTGTGAGCTCCAGTCCATCCGGGAGGGCGGTGTCTTCGAGCTGCGGCAGGGC 479

Qy         146 AspThr------IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThr 163
               |||         :::::::::      ::::::          |||          ||||||
Db         480 GACATGGTCTTTGTCAATGTGACGGACTCAACAGCAGTGAACGTCAACCCTGGCAACACC 539

Qy         164 TyrTrpGlyIleIleLeuLeu 170
               |||:::|||:::       |||
Db         540 TACTTTGGCATGTTCAAGCTG 560

RESULT 12
CC250868
LOCUS       CC250868               1514 bp    DNA     linear   GSS 13-MAY-2003
DEFINITION  CH261-17B4_Sp6.1 CH261 Gallus gallus genomic clone CH261-17B4,
            genomic survey sequence.
ACCESSION   CC250868
VERSION     CC250868.1  GI:30587618
KEYWORDS    GSS.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1514)
  AUTHORS   Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
            Warren,W., Graves,T., Mardis,E. and Wilson,R.
  TITLE     Gallus gallus BAC End Reads
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 182000   Std Error: 0.00
            Seq primer: Sp6 ATTTAGGTGACACTATAG
            Class: BAC ends
            High quality sequence start: 326
            High quality sequence stop: 920.
FEATURES             Location/Qualifiers
     source          1. .1514
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /strain="Red Jungle Fowl"
                     /db_xref="taxon:9031"
                     /clone="CH261-17B4"
                     /sex="female"
                     /cell_line="UCD001, inbred 256"
                     /clone_lib="CH261"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CH261 Female Chicken library - for library and clone
                     ordering information: http://www.chori.org/bacpac"
ORIGIN

Alignment Scores:
Pred. No.:                3.49           Length:          1514
Score:                    96.00          Matches:         45
Percent Similarity:       37.95%         Conservative:    18
Best Local Similarity:    27.11%         Mismatches:      54
Query Match:              10.09%         Indels:          50
DB:                       28             Gaps:            7

US-09-195-368-1 (1-177) x CC250868 (1-1514)

Qy           6 LeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAla---GlnArgSerSerTrp 24
               |||         |||   :::|||||||||   :::|||:::         |||||||||
Db         674 TTGAACACTTTTCCTGCTACACACAGTAGGAATAAGGGGTCTTGGTGGATTTCCAGTTGG 733

Qy          25 LysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeu 44
```

```
Db        734 TCTTTCTTTCTGATGCTGTCCTTTCTCTTTCTTTCCTTC---------------------- 772

Qy         45 IlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyPro 64

Db        773 ---------TTTCTCTCTCTCTCCATTGCT---------TGTGTG--------------- 799

Qy         65 LeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAsp 84

Db        800 ------------------------------------TGTAC-ACACGTGTGTCTGAT 819

Qy         85 TrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsn 104

Db        820 --------------------------------GTGATATATGGATGTGTGGTTCCCTCT 846

Qy        105 AlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIle 124

Db        847 GCTGTAGAGGGAGAGTATTGCCCTTGGGAGAAAGAGCTTCAGCAAGGCCTC---TGGCTT 903

Qy        125 GlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisVal 144

Db        904 CAACGTCTCTCAAATGAAGAGGACACGGGTACATTTAAAGGTACCCATATGCTA------ 957

Qy        145 GlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyr 164

Db        958 ---------TTTCCACTTCCCCTAAATATGGGGGGAATGTTTTTAAAGAACAGGTCCCAT 1008

Qy        165 TrpGlyIleIleLeuLeu 170

Db       1009 ACCAAGAAGATTCTGCTG 1026
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RESULT 13
BX709408

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LOCUS       BX709408                842 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX709408 XGC-tadpole Silurana tropicalis cDNA clone TTpA007c07 5',
            mRNA sequence.
ACCESSION   BX709408
VERSION     BX709408.1  GI:38371615
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 842)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA007c07.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .842
                     /organism="Silurana tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA007c07"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN
```

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.65 | Length: | 842 |
| Score: | 95.50 | Matches: | 53 |
| Percent Similarity: | 49.20% | Conservative: | 39 |
| Best Local Similarity: | 28.34% | Mismatches: | 72 |
| Query Match: | 10.04% | Indels: | 25 |
| DB: | 13 | Gaps: | 10 |

US-09-195-368-1 (1-177) x BX709408 (1-842)

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Qy          9 MetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTrpLysLeuTrpLeu 28

Db         85 ATGCCA---ACACCACAAAGGCCACAGGCAGCATCCAAATCCAAATGGAGCATCTTTCAC 141

Qy         29 PheCysSerIle-ValMetLeu------LeuPheLeuCysSerPheSerTrpLeuIlePh 46

Db        142 ATTTGTACAATTTGTACTTTTGTGCTCTCTGTGGCTGTGCTTGCATTCTGCCTTGCTTTT 201

Qy         46 eIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuPr 66

Db        202 CACCAGGCTAAATATCTCACTGTGTGCAGTTCCAAA----GCTAAATGGGCTCCAGATTC 257

Qy         66 oSerLysTrpGlnMetAlaSerSerGlu---ProProCysValAsn-LysValSerAspT 85

Db        258 AAACACATGGCT-ATGGAGACCCAAGAAGTGCAGCCTAGAGTGGCTCAAGGCGAACAACT 316

Qy         85 rpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnA 105

Db        317 CGACAGTGGAAATAAACATAACAGGCTTTTACATGATCCACATCCAAGTATCCTACTCTG 376

Qy        105 laAsn---TyrAsnAspValAlaPro---------PheGluValArgLeuTyr------- 118

Db        377 TGTCTTTACAAAATGGCATGGTGCCAAAGTCTCAGATTGAGCTAAAAGTGCTTTGTGATG 436

Qy        119 -----LysAsnLysAspMetIleGlnThrLeu--------------ThrAsnLysSerL 132

Db        437 GTTCTTCACAGAAAAATATAATAAGGGAAGTCTTTTTCACAGATACTGCTAATCAAAAAA 496

Qy        132 ysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeu---I 151

Db        497 AAATTGTTACATTAGATGCATCTGCTCTGCTAATGAAAGGAAACAAAATCCAACTTCATA 556

Qy        151 lePheAsnSerGluHisGlnValLeuLysAsnAsn------ThrTyrTrpGlyIleIleL 169

Db        557 TAGAAGGACATACAAATGCTATTTTGGTACATGATAGTTTAACTTTCTGGGAAATAAATG 616

Qy        169 euLeuAlaAsnProGln 174

Db        617 CAATTACCGGTCCTGAA 633
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RESULT 14
CC508168

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LOCUS       CC508168                808 bp    DNA     linear   GSS 17-JUN-2003
DEFINITION  CH240_350K10.T7 CHORI-240 Bos taurus genomic clone CH240_350K10,
            genomic survey sequence.
ACCESSION   CC508168
VERSION     CC508168.1  GI:31826461
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 808)
  AUTHORS   Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
            Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
            Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
            Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
            Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
```

```
            Dalrymple,B.P. and Tellam,R.
  TITLE     Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: CH240_350K10.TARBAC13P2
            Contact: Rob Holt
            Sequencing
            The British Columbia Cancer Agency Genome Science Centre
            600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
            Tel: 604-877-6085
            Fax: 604-877-6276
            Email: rholt@bcgsc.ca
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
            British Columbia Genome Sciences Centre, Canada.
            Plate: 350  row: K  column: 10
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .808
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_350K10"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:                3.09          Length:          808
Score:                    93.00         Matches:         41
Percent Similarity:       38.46%        Conservative:    24
Best Local Similarity:    24.26%        Mismatches:      36
Query Match:              9.78%         Indels:          68
DB:                       29            Gaps:            10

US-09-195-368-1 (1-177) x CC508168 (1-808)

Qy          9 MetProLeuSerHisSerArgThrGln---------------------------------- 17
              :::|||||||||   :::   |||
Db        344 CTCCCTCTTTCTCTTGCAGGAACACCTGGGCAGCTCTCCTTGAAGGGGATGCAGTGCTCT 403

Qy         18 ------GlyAlaGlnArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeu 35
                  |||   :::|||:::   |||:::                |||||
Db        404 GCGTGTGGCCTGGAGCGGGCAGGCTGGCAG------------TGCTCC------------ 439

Qy         36 LeuPheLeuCysSerPheSerTrpLeuIlePheIlePheLeuGlnLeuGluThr------ 53
                        |||:::||||||||:::::   ||||||:::|||   :::
Db        440 ------------TCCTGGAGCTGGCTGCTCTGGCAGTTTCTGCGTCTCTCCAGCCTCTTT 487

Qy         54 ------------------------AlaLysGluProCysMetAlaLysPheGly------ 63
                                     :::|||      |||         |||
Db        488 CTGTCTGATCTCCTCTGGGGGTTTCAGGAGGAGCTGAAGATGGGGATTCTGGGGAATGAC 547

Qy         64 --------------------------ProLeuProSerLysTrp---------GlnMet 71
                                        |||||||||   :::|||         |||
Db        548 TTTTACCTTTGGTGGGTGCAGGGCACCCCTCTGCCTGGGAGGTGGAGAAGGGGGCAGACC 607

Qy         72 AlaSerSerGluProPro---------CysValAsnLysValSerAspTrpLysLeuGlu 88
              :::|||   ||||||||         |||:::   :::|||      |||
Db        608 TCAAGTGGGGAGCCACCTGGGCTGAGGTGCCTGGGCCAAGTTAGACCTTGG--------- 658

Qy         89 IleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyrAsn 108
                        ||||||            |||      ||||||
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```
Db        659 ------------GGCCTGAAGGCTTCTGGTGGGTAGCCGGCCCCC--------------- 691

Qy        109 AspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThr 128
                     :::|||   :::   |||      :::::::::      :::   :::
Db        692 ------TCCCCACTGAAGCACCGAGCTCTAAGAAGTCAAACACGTGTTGACTCATTTGTT 745

Qy        129 AsnLysSerLysIleGlnAsnValGly 137
                    :::||||||   :::|||
Db        746 ------GGAGAAATTCAGCTCATGGGC 766

RESULT 15
BU996000
LOCUS       BU996000                506 bp    mRNA    linear   EST 23-OCT-2002
DEFINITION  HM12B02r HM Hordeum vulgare subsp. vulgare cDNA clone HM12B02
            5-PRIME, mRNA sequence.
ACCESSION   BU996000
VERSION     BU996000.1  GI:24272983
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
  TITLE     EST sequencing and analysis in barley (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466, Gatersleben, Germany
            Tel: 039482-5522
            Fax: 039482-5595
            Email: stein@ipk-gatersleben.de
            Insert Length: 506   Std Error: 0.00
            Plate: 12  row: B  column: 2
            Seq primer: M13rev.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:255878"
                     /db_xref="taxon:112509"
                     /clone="HM12B02"
                     /tissue_type="male inflorescences"
                     /dev_stage="male inflorescences (approx. 2 mm in size),
                     green anther stage"
                     /lab_host="XL10-Gold"
                     /clone_lib="HM"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
                     cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
                     artefact caused by the kit, in most cases the EcoRI site
                     is NOT present, as well as the EcoRIadapter used for
                     cloning. To excise the insert, restriction sites upstream
                     EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also
                     due to the cloning system used Blue/white selection for
                     recombinats is not 100% reliable."
ORIGIN

Alignment Scores:
Pred. No.:                2.3           Length:          506
Score:                    91.50         Matches:         36
Percent Similarity:       45.13%        Conservative:    15
Best Local Similarity:    31.86%        Mismatches:      54
Query Match:              9.62%         Indels:          8
DB:                       13            Gaps:            3

US-09-195-368-1 (1-177) x BU996000 (1-506)

Qy          1 MetCysLeuSerHisLeuGluAsn-MetProLeuSerHisSerArgThrGlnGlyAlaGl 20
              :::||||||   |||   |||||| :::      |||:::   :::      |||:::
```

```
Db         23 CTCTGCCTCCTACATAGAGAAAACAGTTTCCTTCTCATACAAGAAAGAGATGGGTTCA-- 80

Qy         20 nArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSe 40
                  ::::::   :::|||      |||   |||   :::|||||||||      |||::
Db         81 ----ACCACCGTCAGGCTCATCGCCTTCGTCTCCGCCCTCATGCTACTCATGCACTGCAC 136

Qy         40 rPheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAla---LysGluProCysMe 59
              :   :::                |||||||||  .    ||||||   |||      |||::
Db        137 TCACGCGGCAGCACCGGCAGCCTTTCTTCAGACACCGACGGCGGTGAAGACGTGGTGCGT 196

Qy         59 tAlaLys-----------PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGl 75
              :||||||                    |||   :::     :::   |||   |||||
Db        197 GGCCAAGCCTTCGACCGGCGAGGCGGCCCTGAGGGCCAACCTGGAGTTCGCCTGCTCCGA 256

Qy         75 uProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTy 95
              |      |||                                    |||      |||:::
Db        257 GAGCGACTGCAGCGCGATCCAGGGCACGGGGGGCTGCTCCGCACTGAACGGCGGCGTGCT 316

Qy         95 rLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 107
               |||            ||||||  ||||||  |||
Db        317 GCTGTCGCGGGCGTCGGTGGCCATGAACGCCTACTAC 353
```

Search completed: April 7, 2004, 19:35:47
Job time : 2440.23 secs

GenCore version 5.1.6


OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:53:26 ; Search time 314.795 Seconds
(without alignments)
2388.639 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENMPLSHSRTQGAQ.....VLKNNTYWGIILLANPQFIS 177

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09195368/runat_07042004_061637_2588/app_query.fasta_1.654
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09195368_@CGN_1_1_886_@runat_07042004_061637_2588 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 951 | 100.0 | 534 | 7 | ACC57580 | Acc57580 Polynucle |
| 2 | 951 | 100.0 | 534 | 7 | ACC57909 | Acc57909 Human GIT |
| 3 | 951 | 100.0 | 534 | 9 | ADC35221 | Adc35221 Human cDN |
| 4 | 951 | 100.0 | 1809 | 2 | AAV19195 | Aav19195 Human end |
| 5 | 951 | 100.0 | 1849 | 3 | AAA74936 | Aaa74936 cDNA enco |
| 6 | 951 | 100.0 | 1849 | 3 | AAZ57314 | Aaz57314 Human end |
| 7 | 951 | 100.0 | 1849 | 8 | ADA11463 | Ada11463 Human end |
| 8 | 951 | 100.0 | 1849 | 9 | ADC01857 | Adc01857 Human cDN |
| 9 | 951 | 100.0 | 1964 | 2 | AAX59844 | Aax59844 cDNA sequ |
| 10 | 951 | 100.0 | 1964 | 2 | AAX87726 | Aax87726 Human PRO |
| 11 | 951 | 100.0 | 1964 | 4 | AAC85435 | Aac85435 Clone PRO |
| 12 | 951 | 100.0 | 1964 | 4 | AAF30051 | Aaf30051 Human cDN |
| 13 | 951 | 100.0 | 1964 | 4 | AAC97374 | Aac97374 Human ang |
| 14 | 951 | 100.0 | 1964 | 4 | AAC85945 | Aac85945 Native se |
| 15 | 951 | 100.0 | 1964 | 4 | AAC90563 | Aac90563 Human PRO |
| 16 | 951 | 100.0 | 1964 | 6 | ABK28562 | Abk28562 Human DNA |
| c 17 | 814 | 85.6 | 1527 | 5 | AAS90614 | Aas90614 DNA encod |
| 18 | 814 | 85.6 | 1527 | 5 | AAS81613 | Aas81613 DNA encod |
| 19 | 281 | 29.5 | 162 | 4 | AAK43619 | Aak43619 Human bon |
| 20 | 170 | 17.9 | 397 | 4 | AAK30610 | Aak30610 Human bon |
| 21 | 107 | 11.3 | 60 | 6 | ABN41382 | Abn41382 Human spl |
| 22 | 92 | 9.7 | 50 | 6 | ABZ02741 | Abz02741 Human leu |
| c 23 | 86.5 | 9.1 | 455 | 8 | ACH41523 | Ach41523 Human foe |
| 24 | 86 | 9.0 | 320 | 6 | ABN18154 | Abn18154 Human ORF |
| c 25 | 86 | 9.0 | 2637 | 6 | ABL40958 | Abl40958 Human tra |
| 26 | 86 | 9.0 | 58708 | 4 | AAK64739 | Aak64739 Human imm |
| 27 | 85.5 | 9.0 | 3515 | 6 | AAD31199 | Aad31199 Human WKL |
| 28 | 85.5 | 9.0 | 3515 | 6 | AAD31200 | Aad31200 Human WKL |
| 29 | 85.5 | 9.0 | 3650 | 4 | AAI58154 | Aai58154 Human pol |
| 30 | 85.5 | 9.0 | 3650 | 8 | ADB48120 | Adb48120 Novel hum |
| 31 | 85.5 | 9.0 | 3912 | 4 | AAI60197 | Aai60197 Human pol |
| 32 | 85.5 | 9.0 | 15690 | 6 | ABK15000 | Abk15000 Canine di |
| 33 | 84.5 | 8.9 | 1008 | 6 | ABI98960 | Abi98960 Canine di |
| 34 | 84.5 | 8.9 | 1727 | 4 | AAS60941 | Aas60941 Human can |
| 35 | 84.5 | 8.9 | 1797 | 6 | ABN66564 | Abn66564 Streptoco |
| 36 | 84.5 | 8.9 | 2641 | 6 | ABZ82536 | Abz82536 Human sec |
| 37 | 84.5 | 8.9 | 3666 | 9 | ADC90678 | Adc90678 E. faeciu |
| 38 | 84.5 | 8.9 | 4042 | 5 | AAS83774 | Aas83774 DNA encod |
| 39 | 84.5 | 8.9 | 15690 | 6 | ABK15038 | Abk15038 Canine di |
| 40 | 84.5 | 8.9 | 18826 | 6 | ABK15039 | Abk15039 Canine di |
| c 41 | 84.5 | 8.9 | 110000 | 6 | ABN71527_07 | Continuation (8 of |
| c 42 | 84 | 8.8 | 569 | 9 | ADD34676 | Add34676 Mouse mit |
| c 43 | 84 | 8.8 | 100301 | 6 | ABQ88176 | Abq88176 Human ost |
| c 44 | 83 | 8.7 | 10697 | 4 | AAK83607 | Aak83607 Human imm |
| c 45 | 83 | 8.7 | 10697 | 5 | ABA21005 | Aba21005 Human ner |

ALIGNMENTS

RESULT 1
ACC57580
ID ACC57580 standard; DNA; 534 BP.
XX
AC ACC57580;
XX
DT 28-JUL-2003 (first entry)
XX
DE Polynucleotide encoding tumour necrosis factor superfamily member.
XX
KW Human; RANKL; tumour necrosis factor; osteopathic; bone; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003033663-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033022.
XX
PR 15-OCT-2001; 2001US-0329393P.
XX
PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI Lam J, Ross PF, Teitelbaum SL;
XX
DR WPI; 2003-430346/40.
XX
PT New RANKL mimic comprising a core, and at least one external loop, useful
PT for enhancing processes of bone formation or inhibiting bone resorption,
PT thus providing treatments for disease or condition characterized by loss
PT of bone mass.

```
XX
PS   Disclosure; Page 58; 78pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a non-RANKL
CC   member of the tumour necrosis factor (TNF) superfamily. The invention
CC   provides non-naturally-occurring proteins that contain one or more of the
CC   external surface loops of RANKL (see ABR42066-70) in combination with a
CC   heterologous protein core obtained from a non-RANKL member of the TNF
CC   superfamily. Also provided are polynucleotides encoding such proteins.
CC   The proteins bind to RANK, acting as mimics of RANKL. They can be used to
CC   enhance bone formation by either inhibiting bone resorption or inducing
CC   osteogenesis, thus providing treatment for diseases or conditions
CC   characterised by loss of bone mass
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.16e-100      Length:          534
Score:                  951.00         Matches:         177
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     7              Gaps:            0

US-09-195-368-1 (1-177) x ACC57580 (1-534)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 2
ACC57909
ID   ACC57909 standard; cDNA; 534 BP.
XX
AC   ACC57909;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human GITRL polynucleotide.
XX
KW   Human; GITRL; tumour necrosis factor; ligand; cytostatic;
KW   immunomodulator; osteopathic; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .534
FT                   /*tag=  a
FT                   /product= "Human GITRL"
XX
PN   WO2003040307-A2.
XX
PD   15-MAY-2003.
XX
PF   25-JUL-2002; 2002WO-US023782.
XX
PR   27-JUL-2001; 2001US-0307838P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Hilbert DH,  Rosen CA;
XX
DR   WPI; 2003-430659/40.
DR   P-PSDB; ABR42323.
XX
PT   New heteromultimeric complex having a first polypeptide member of the
PT   tumor necrosis factor (TNF) ligand family, and a second different member
PT   of TNF ligand family, useful for treating cancer, osteoporosis or an
PT   autoimmune disease.
XX
PS   Disclosure; Page 382; 388pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding human GITRL.
CC   The invention relates to compositions comprising heterotrimeric complexes
CC   of tumour necrosis factor (TNF) ligand family members, and their use in
CC   the detection, prevention and treatment of disease. In preferred
CC   embodiments, the heterotrimeric complex comprises full-length or
CC   extracellular portions of GITRL together with full-length or
CC   extracellular portions of other TNF ligand family members. The
CC   heterotrimeric complexes of the invention are useful for treating an
CC   autoimmune disease, cancer or osteoporosis, and particularly for
CC   inhibiting cancer cell proliferation, increasing B cell proliferation, or
CC   inducing apoptosis of T cells
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.16e-100      Length:          534
Score:                  951.00         Matches:         177
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     7              Gaps:            0

US-09-195-368-1 (1-177) x ACC57909 (1-534)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 3
ADC35221
ID   ADC35221 standard; cDNA; 534 BP.
XX
AC   ADC35221;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cDNA encoding TNF ligand family member #20.
XX
KW   ss; gene; human; tumour necrosis factor; TNF ligand; endokine alpha;
KW   excessive bone resorption disorder; osteoporosis; Paget's disease;
KW   arterial calcification.
XX
OS   Homo sapiens.
XX
PN   US2003100074-A1.
XX
PD   29-MAY-2003.
XX
PF   15-AUG-2002; 2002US-00218547.
XX
PR   16-AUG-2001; 2001US-0312542P.
PR   30-OCT-2001; 2001US-0330761P.
XX
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (NARD/) NARDELLI B.
XX
PI   Yu G,  Ni J,  Rosen CA,  Nardelli B;
XX
DR   WPI; 2003-696072/66.
DR   P-PSDB; ADC35222.
XX
PT   New Endokine alpha gene useful for preparing a composition for treating a
PT   disease associated with excessive or insufficient bone resorption e.g.,
PT   osteoporosis, Paget's disease or arterial calcification.
XX
PS   Disclosure; SEQ ID NO 39; 145pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule encoding a
CC   tumour necrosis factor family ligand. A composition comprising the
CC   isolated antibody or its fragment is used for treating an individual in
CC   need of decreased level of endokine alpha activity. The endokine alpha
CC   polypeptide present in a heterotrimeric complex is used for treating an
CC   individual having a disorder associated with excessive bone resorption,
CC   e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC   individual having a disorder associated with insufficient bone resorption
CC   comprises administering an endokine alpha antagonist, which is the
CC   antibody that binds specifically to endokine alpha polypeptide. The
CC   present sequence represents a cDNA encoding a tumour necrosis factor
CC   family ligand.
XX
SQ   Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                2.16e-100       Length:          534
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-09-195-368-1 (1-177) x ADC35221 (1-534)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 4
AAV19195
ID   AAV19195 standard; cDNA; 1809 BP.
XX
AC   AAV19195;
XX
DT   28-AUG-1998  (first entry)
XX
DE   Human endokine-alpha cDNA.
XX
KW   Endokine-alpha; cytokine; tumour necrosis factor; human;
KW   immunomodulation; infection; cell proliferation; angiogenesis; tumour;
KW   metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;
KW   diagnosis; therapy; ds; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
XX
PN   WO9807880-A1.
XX
PD   26-FEB-1998.
XX
PF   16-AUG-1996;   96WO-US013282.
```

```
XX
PR   16-AUG-1996;   96WO-US013282.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 1998-169182/15.
DR   P-PSDB; AAW37847.
XX
PT   Nucleic acid encoding human endokine-alpha - useful for diagnosis and
PT   treatment of tumour necrosis factor-related diseases.
XX
PS   Claim 1; Fig 1A-B; 78pp; English.
XX
CC   This isolated nucleic acid, deposited as ATCC 97640, codes for human
CC   endokine-alpha (see AAW37847), a novel member of the tumour necrosis
CC   factor (TNF) family of cytokines. It was isolated from a cDNA library
CC   established from human striatum. Expressed sequence tags corresponding to
CC   a portion of the endokine-alpha cDNA were also found in several
CC   endothelial libraries and a foetal liver library. Isolation of the
CC   nucleic acid allows production of recombinant endokine-alpha in
CC   transformed host cells. Endokine-alpha may be involved in disorders of
CC   immunomodulation, infection, cell proliferation, angiogenesis, tumour
CC   metastasis, apoptosis, sepsis and endotoxaemia, and may be useful for
CC   treating melanoma and sarcoma. A claimed diagnostic method comprises
CC   assaying endokine-alpha gene expression as a means of detecting a TNF-
CC   related disorder. Fragments of endokinase-alpha nucleic acids can be used
CC   as probes, e.g. for fluorescent in situ hybridisation, for identifying
CC   genomic or other related sequences and in chromosome identification
XX
SQ   Sequence 1809 BP; 549 A; 355 C; 351 G; 554 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.25e-99        Length:          1809
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       2               Gaps:            0

US-09-195-368-1 (1-177) x AAV19195 (1-1809)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTGGCAAATCCCCAATTCATCTCC 559

RESULT 5
AAA74936
ID   AAA74936 standard; cDNA; 1849 BP.
XX
AC   AAA74936;
XX
DT   02-JAN-2001  (first entry)
XX
DE   cDNA encoding a human endokine-alpha polypeptide.
XX
KW   Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
KW   chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
KW   autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
KW   acute inflammation; acute allograft rejection; graft versus host disease;
KW   transplant rejection; foetal resorption; faecal peritonitis;
KW   bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemeia;
KW   polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
KW   chronic active hepatitis; myasthenia gravis; psoriasis; vitilogo;
KW   Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
KW   pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
KW   discoid lupus; dense deposit disease; endocrine ophthalmopathy;
KW   irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;
KW   juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
KW   lymphopenias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
KW   primary myxedema; polymyositis; mixed connective tissue disease;
KW   keratoconjunctivitis sicca; vernal keratoconjunctivitis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
FT                   /product= "endokine-alpha"
XX
PN   WO200050620-A2.
XX
PD   31-AUG-2000.
XX
PF   25-FEB-2000; 2000WO-US004722.
XX
PR   26-FEB-1999;   99US-0122099P.
PR   28-MAY-1999;   99US-0136788P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 2000-572097/53.
DR   P-PSDB; AAB08785.
XX
PT   Polynucleotide encoding endokine alpha protein, which is a member of
PT   tumor necrosis factor useful for treating inflammatory diseases,
PT   disorders such as cancer, allergy, diabetes and various neurological
PT   disorders.
XX
PS   Claim 5; Fig 1; 263pp; English.
XX
CC   The present sequence encodes a human endokine-alpha polypeptide. The
CC   polypeptide is a cytokine which is similar to tumour necrosis factor
CC   (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC   treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC   autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC   inflammation, acute inflammation, acute allograft rejection, graft versus
CC   host disease, transplant rejection, foetal resorption, faecal
CC   peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC   hypergammaglobulinemeia, polychondritis, scleroderma, Wegener
CC   granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
```

```
CC   gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitilogo,
CC   gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC   bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC   ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC   sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC   mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC   syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
CC   connective tissue disease, keratoconjunctivitis sicca, and vernal
CC   keratoconjunctivitis,
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.29e-99        Length:         1849
Score:                    951.00          Matches:        177
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-09-195-368-1 (1-177) x AAA74936 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 6
AAZ57314
ID   AAZ57314 standard; cDNA; 1849 BP.
XX
AC   AAZ57314;
XX
DT   03-APR-2000  (first entry)
XX
DE   Human endokine alpha protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KW   immunomodulation; inflammation; cell proliferation; angiogenesis;
KW   tumour metastasis; apoptosis; sepsis; endotoxemia; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
FT                   /product= "endokine alpha"
XX
PN   US5998171-A.
XX
PD   07-DEC-1999.
XX
PF   15-AUG-1997;   97US-00912227.
XX
PR   16-AUG-1996;   96US-0024058P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Rosen CA,  Yu G;
XX
DR   WPI; 2000-104608/09.
DR   P-PSDB; AAY53061.
XX
PT   Isolated human endokine alpha gene useful as a diagnostic probes and
PT   primers.
XX
PS   Claim 3; Fig 1; 31pp; English.
XX
CC   The present sequence encodes human endokine alpha which is a member of
CC   the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC   protein and polynucleotides can be used in diagnostic and therapeutic
CC   methods concerning TNF family-related disorders. These include disorders
CC   associated with immunomodulation and inflammation, cell proliferation,
CC   angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.29e-99        Length:         1849
Score:                    951.00          Matches:        177
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       3               Gaps:           0

US-09-195-368-1 (1-177) x AAZ57314 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448
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Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 7
ADA11463
ID   ADA11463 standard; cDNA; 1849 BP.
XX
AC   ADA11463;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human endokine alpha cDNA.
XX
KW   human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;
KW   infection; viral; bacterial; yeast; fungal; Toxoplasma gondii;
KW   Schistosoma mansoni; Listeria monocytogenes; tumour necrosis factor;
KW   TNF-related disorder; endokine alpha-related disorder; immunomodulation;
KW   inflammation; cell proliferation; angiogenesis; tumour metastasis;
KW   apoptosis; sepsis; endotoxaemia; ss; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag=  a
FT                   /product= "Endokine alpha"
XX
PN   US2002099198-A1.
XX
PD   25-JUL-2002.
XX
PF   01-JUL-1999;   99US-00345790.
XX
PR   16-AUG-1996;   96US-0024058P.
PR   15-AUG-1997;   97US-00912227.
XX
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 2003-605663/57.
DR   P-PSDB; ADA11464.
XX
PT   Novel isolated endokine alpha polypeptide, a member of tumor necrosis
PT   factor ligand family, and antibodies against the polypeptides, useful for
PT   treating melanoma, sarcoma, and viral, bacterial, fungal infections.
XX
PS   Claim 5; Fig 1; 29pp; English.
XX
CC   The invention relates to an isolated human endokine alpha polypeptide. A
CC   cell recombinant for the human endokine alpha polypeptide is useful for
CC   producing the protein by recombinant techniques. The antigenic epitope
CC   bearing peptides and polypeptides are useful to raise antibodies
CC   including monoclonal antibodies. The peptides and antipeptide antibodies
CC   are used in a variety of qualitative or quantitative assays for the
CC   protein. The protein is useful for tumour targeting and thus used in
CC   patients with melanoma and sarcoma for tumour regression and extension of
CC   patient life-span through a local injection. the protein is also useful
CC   for treating viral, bacterial, yeast, fungal and other infections e.g.,
CC   Toxoplasma gondii, Schistosoma mansoni, Listeria monocytogenes etc. The
CC   protein is also useful for treating other tumour necrosis factor (TNF)-
CC   related disorders. The nucleic acid is useful as probes for gene mapping
CC   by in situ hybridisation and for detecting expression of endokine alpha
CC   gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
CC   also useful for diagnosing an endokine alpha-related disorder such as
CC   disorders associated with immunomodulation and inflammation, cell
CC   proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
CC   endotoxaemia. The antibody is useful diagnostically or therapeutically as
CC   antagonists in the treatment of alpha and/or TNF-related disorders. The
CC   antibody is also useful for purification of the protein. The antibodies
CC   are useful for detecting the protein and for tracking the fate of various
CC   regions of a protein precursor which undergoes post-translational
CC   processing. The present sequence represents cDNA encoding human endokine
CC   alpha.
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.29e-99        Length:          1849
Score:                    951.00          Matches:         177
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       8               Gaps:            0

US-09-195-368-1 (1-177) x ADA11463 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 8
ADC01857
ID   ADC01857 standard; cDNA; 1849 BP.
XX
AC   ADC01857;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cDNA encoding Endokine alpha.
XX
KW   Human; ss; gene; endokine alpha; tumour necrosis factor family; AIDS;
KW   chronic lymphocyte disorder; tumour; parasitic disease;
KW   autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
KW   graft versus host disease; transplant rejection; skin allergy;
KW   bowel disease; wound; sepsis; Hodgkin's disease;
KW   chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;
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KW   chronic active hepatitis; myasthenia gravis; psoriasis;
KW   autoimmune thyroiditis; Goodpasture's disease; asthma; Graves disease;
KW   cirrhosis; insulin dependent diabetes mellitus; Sjogren's syndrome;
KW   glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
KW   rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53. .562
FT                   /*tag= a
FT                   /product= "Endokine alpha"
XX
PN   US2002168729-A1.
XX
PD   14-NOV-2002.
XX
PF   02-MAY-2002; 2002US-00136511.
XX
PR   16-AUG-1996;   96US-0024058P.
PR   15-AUG-1997;   97US-00912227.
PR   26-FEB-1999;   99US-0122099P.
PR   28-MAY-1999;   99US-0136788P.
PR   01-JUL-1999;   99US-00345790.
PR   25-FEB-2000; 2000US-00513584.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Yu G,  Ni J,  Rosen CA;
XX
DR   WPI; 2003-755028/71.
XX
PT   Novel isolated endokine alpha polypeptide AIDS, chronic lymphocyte
PT   disorder, common variable immunodeficiency, a tumor, parasitic disease,
PT   autoimmune disease, lupus, arthritis, multiple sclerosis.
XX
PS   Claim 1; SEQ ID NO 1; 90pp; English.
XX
CC   The invention relates to an isolated endokine alpha polypeptide (a member
CC   of the tumour necrosis factor family), appearing as ADC01858, the
CC   sequence of the endokine alpha polypeptide having an sequence encoded by
CC   the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
CC   sequence of an epitope-bearing portion of the above polypeptides. Also
CC   included are the encoding nucleic acid (its homologues, complements or
CC   fragments where the fragment comprises at least 50 contiguous
CC   nucleotides), provided that the fragment is not from a region starting at
CC   nucleotide 26 and ending at nucleotide 476 of ADC01857), making a
CC   recombinant vector comprising the nucleic acid and an isolated antibody
CC   or antibody fragment that binds specifically to endokine alpha. The DNA
CC   and protein are useful for treating an individual having a disorder
CC   chosen from AIDS, chronic lymphocyte disorder, common variable
CC   immunodeficiency, a tumour, parasitic disease, autoimmune disease, lupus,
CC   arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
CC   chronic inflammation, acute inflammation, acute allograft rejection,
CC   graft versus host disease, transplant rejection, foetal resorption,
CC   faecal peritonitis, skin allergies, bowel disease, a wound, sepsis, ALL,
CC   Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocyte leukaemia,
CC   plasmacytomas, multiple myeloma, Burkitt's lymphoma, EBV-transformed
CC   disease, chronic myelogenous leukaemia, chronic hypergammaglobulinaemeia,
CC   autoimmune haematological disorders, polychondritis, scleroderma, Wegener
CC   granulomatosis, dermatomyosisitis, chronic active hepatitis, myasthenia
CC   gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, autoimmune
CC   thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
CC   enteropathy, autoimmune neutropenias, pemphigus vulgaris, Goodpasture's
CC   disease, bullous pemphigoid, discoid lupus, dense deposit disease,
CC   endocrine ophthalmopathy, IBD, asthma, Graves disease, Sarcoidosis,
CC   cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
CC   uveitis, autoimmune gastritis, lymphopaenias, olyarteritis nodosa,
CC   Sjogren's syndrome, Bechet's disease, Hashimoto's disease, primary
CC   myxedema, polymyositis, mixed connective tissue disease,
CC   keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
CC   lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
CC   anaemia, contact sensitivity disease, Parkinson's disease, primary
CC   lateral sclerosis, silicosis, sarcoidosis, idiopathic pulmonary fibrosis,
CC   idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis,
CC   histamine-mediated allergic reactions, IgE-mediated allergic reactions,
CC   rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
CC   present sequence encodes Endokine alpha.
XX
SQ   Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.29e-99        Length:         1849
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1 (1-177) x ADC01857 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 9
AAX59844
ID   AAX59844 standard; cDNA; 1964 BP.
XX
AC   AAX59844;
XX
DT   28-JUL-1999  (first entry)
XX
DE   cDNA sequence for human DNA19355.
XX
KW   DNA19355; tumour necrosis factor homologue; receptor GITR; immunogen;
KW   antibody; apoptosis; mammalian cancer cell;
KW   tumour necrosis factor (TNF)-alpha secretion; primary T- cell;
KW   proinflammatory response; ds.
XX
OS   Homo sapiens.
XX
PN   WO9925834-A1.
XX
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PD   27-MAY-1999.
XX
PF   18-NOV-1998;   98WO-US024621.
XX
PR   18-NOV-1997;   97US-0065635P.
PR   12-DEC-1997;   97US-0069661P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti R,  Baker KP;
PI   Godowski PJ,  Mark MR;
XX
DR   WPI; 1999-338009/28.
DR   P-PSDB; AAY15817.
XX
PT   New DNA19355 polypeptide as tumour necrosis factor homolog.
XX
PS   Example 1; Fig 1; 86pp; English.
XX
CC   The present sequence encodes a polypeptide designated DNA19355. The
CC   polypeptide is a tumour necrosis factor homologue. The DNA19355
CC   polynucleotide sequence can be used to derive hybridisation probes for
CC   e.g. isolating similar sequences, gene mapping, genetic analysis, etc.
CC   Nucleic acids which encode DNA19355 can also be used to generate
CC   transgenic or knockout animals, which are useful in the development and
CC   screening of therapeutically useful reagents. The DNA19355 polypeptides
CC   may be used in diagnostic assays to detect the presence of the receptor
CC   GITR in mammalian tissues. The polypeptides can also be used as
CC   immunogens to raise antibodies. The polypeptides may also be used to
CC   induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
CC   stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
CC   cells, and so can be used to stimulate a proinflammatory response in
CC   mammalian cells
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                1.4e-99        Length:          1964
Score:                    951.00         Matches:         177
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

US-09-195-368-1 (1-177) x AAX59844 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
AAX87726
ID   AAX87726 standard; cDNA; 1964 BP.
XX
AC   AAX87726;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human PRO364 ligand cDNA clone DNA19355-1150.
XX
KW   PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
KW   inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
KW   therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             21. .554
FT                   /*tag=  a
XX
PN   WO9940196-A1.
XX
PD   12-AUG-1999.
XX
PF   09-FEB-1999;   99WO-US002642.
XX
PR   09-FEB-1998;   98US-0074087P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti RM,  Wood WI;
PI   Goddard A;
XX
DR   WPI; 1999-494296/41.
DR   P-PSDB; AAY06646.
XX
PT   Tumor necrosis factor receptor homologue - useful for, e.g. modulating
PT   apoptosis and NF-KB activation and proinflammatory or autoimmune
PT   responses.
XX
PS   Example 2; Fig 5A-B; 104pp; English.
XX
CC   This is the nucleotide sequence of a novel cDNA clone, termed DNA19355-
CC   1150 (ATCC 209466), coding for a potential ligand (see AAY06646) of
CC   PRO384 (see AAY06605), a novel member of the tumour necrosis factor
CC   receptor family. The clone was isolated from a human umbilical vein
CC   endothelial cell cDNA library constructed in yeast transformants. PRO364
CC   polypeptides are useful for modulating apoptosis, NF-KB activation and
CC   proinflammatory or autoimmune responses in mammalian cells (claimed)
XX
SQ   Sequence 1964 BP; 596 A; 370 C; 380 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                1.4e-99        Length:          1964
Score:                    951.00         Matches:         177
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       2              Gaps:            0

US-09-195-368-1 (1-177) x AAX87726 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40

Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60

Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80

Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100

Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120

Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140

Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160

Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177

Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551
```

RESULT 11
AAC85435
ID AAC85435 standard; cDNA; 1964 BP.
XX
AC AAC85435;
XX
DT 08-MAY-2001 (first entry)
XX
DE Clone PRO175-1150.
XX
KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR;
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW age-related macular degeneration; antibody; periodontal disease;
KW vascular-related drug targeting; atherosclerosis; hypertension;
KW inflammatory vasculitides; Reynaud's disease; aneurysm;
KW arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
KW fibrosis; neuropathy; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 21. .554
FT /*tag= a
FT /product= "PRO175"
XX
PN WO200103720-A2.
XX
PD 18-JAN-2001.
XX
PF 11-JUL-2000; 2000WO-US018867.
XX
PR 12-JUL-1999; 99US-0143304P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Williams PM, Gerritsen ME;
XX
DR WPI; 2001-138257/14.
DR P-PSDB; AAB47056.
XX
PT Composition for diagnosing and treating cardiovascular, endothelial and
PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX
PS Example 2; Fig 5; 76pp; English.
XX
CC This sequence encodes a PRO175 polypeptide, which is a human gluco-
CC corticoid-induced tumor necrosis factor ligand (hGITRL). The
CC corresponding receptor (hGITR), PRO364, is given in AAB47054. PRO364 and
CC PRO175 may be used in a mixture with a cardiovascular, endothelial,
CC angiogenic or angiostatic agent for the treatment of a cardiovascular,
CC endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was
CC isolated from an expressed sequence tag (EST) database as having homology
CC to members of the tumour necrosis factor receptor (TNFR) family of
CC polypeptides. The PRO175 cDNA sequence was isolated from a library of
CC cDNA fragments derived from human umbilical vein endothelial cells
CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
CC antagonists is useful for treating cardiac hypertrophy (which is
CC initiated by myocardial infarction and characterized by the presence of
CC an elevated level of PGF_2alpha), trauma, a cancer, or age-related
CC macular degeneration in a human. Administering a therapeutically
CC effective amount of an antibody that binds PRO364 or PRO175 is useful for
CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
CC from a tumor or a retinal disorder. PRO364 or PRO175, or their
CC antagonists, are useful for vascular-related drug targeting or as
CC therapeutic targets for the treatment or prevention of atherosclerosis,
CC hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
CC arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
CC or regeneration and treatment of lung or liver fibrosis, periodontal
CC diseases, attraction of bone-forming cells, central and peripheral
CC nervous system disease and neuropathies and rheumatoid arthritis
XX
SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.4e-99 | Length: | 1964 |
| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-195-368-1 (1-177) x AAC85435 (1-1964)

```
Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20

Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40

Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60

Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80

Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100

Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120

Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140

Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440
```

```
Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 12
AAF30051
ID   AAF30051 standard; cDNA; 1964 BP.
XX
AC   AAF30051;
XX
DT   30-APR-2001  (first entry)
XX
DE   Human cDNA encoding PRO175.
XX
KW   PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;
KW   antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW   antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW   dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW   immunostimulant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             21. .554
FT                   /*tag=  a
FT   sig_peptide     21. .152
FT                   /*tag=  b
FT   mat_peptide     153. .551
FT                   /*tag=  c
XX
PN   WO200105972-A1.
XX
PD   25-JAN-2001.
XX
PF   15-MAR-2000; 2000WO-US006884.
XX
PR   20-JUL-1999;   99US-0144758P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Fong S,  Goddard A,  Godowski PJ;
PI   Gurney AL,  Hillan KJ,  Mark MR,  Marsters SA,  Pitti RM,  Tumas D;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-103149/11.
DR   P-PSDB; AAB20109.
XX
PT   New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT   diagnosing and treating immune-related disorders, such as multiple
PT   sclerosis, rheumatoid arthritis and diabetes.
XX
PS   Claim 21; Fig 3; 127pp; English.
XX
CC   The present sequence is that of cDNA clone DNA19355-1150 (ATCC 209466)
CC   encoding novel human immunomodulator protein PRO175 (UNQ149) (see
CC   AAB20109). The clone was isolated from a yeast screening of human cDNA.
CC   The predicted protein (20 kDa, pI 8.08) shows homology to members of the
CC   tumour necrosis factor family. The invention provides polynucleotides
CC   (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
CC   including PRO175. Claimed compositions comprising these proteins or their
CC   agonists are useful for increasing infiltration of inflammatory cells
CC   into a tissue of a mammal, stimulating or enhancing an immune response in
CC   a mammal, or increasing the proliferation of T-lymphocytes in a mammal in
CC   response to an antigen. Claimed compositions comprising the PRO
CC   polypeptide or its antagonist have the opposite effect. A claimed method
CC   for treating an immune related disorder, such as a T cell disorder,
CC   involves administering the PRO polypeptide, an agonist antibody or an
CC   antagonist antibody. The disorder is selected from systemic lupus
CC   erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC   arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
CC   inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC   sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC   thyroiditis, diabetes mellitus, immune-mediated renal disease,
CC   demyelinated diseases (such as multiple sclerosis), autoimmune chronic
CC   active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,
CC   sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis
CC   and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,
CC   (auto)immune-mediated skin diseases (such as bullous skin disease,
CC   erythema multiforme and psoriasis), allergic diseases (such as asthma,
CC   allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC   urticaria), immunologic diseases of the lung and transplantation
CC   associated diseases (such as graft rejection and graft-versus-host
CC   disease) (all claimed). Claimed methods of diagnosing these disorders
CC   comprise detecting the level of expression of the PRO gene. Also claimed
CC   are a method of identifying a compound capable of inhibiting the
CC   expression or activity of the PRO polypeptide, vectors, host cells,
CC   antibodies, and a method of stimulating an immune response in a mammal
CC   using PRO179
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              1.4e-99        Length:         1964
Score:                  951.00         Matches:        177
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     4              Gaps:           0

US-09-195-368-1 (1-177) x AAF30051 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 13
AAC97374
ID   AAC97374 standard; cDNA; 1964 BP.
XX
```

AC AAC97374;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO175 cDNA, SEQ ID NO:8.
XX
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
PF 05-JAN-2000; 2000WO-US000219.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR; Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR P-PSDB; AAB53065.
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiogenic
PT disorders, such as atherosclerosis, wounds or cancer.
XX
PS Claim 58; Fig 3A-B; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to screen
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
CC therapy. PRO nucleic acids can also be used to produce transgenic animals
CC useful for the development and screening of potential therapeutic agents.
CC The present sequence represents a cDNA encoding a PRO protein of the
CC invention
XX
SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.4e-99 | Length: | 1964 |
| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-195-368-1 (1-177) x AAC97374 (1-1964)

```
Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551
```

RESULT 14
AAC85945
ID AAC85945 standard; cDNA; 1964 BP.
XX
AC AAC85945;
XX
DT 22-AUG-2001 (first entry)
XX
DE Native sequence of PRO175 cDNA, clone DNA19355-1150-1.
XX
KW PRO; type II transmembrane protein; tumour necrosis factor; stroke;
KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;

```
KW   myocardial infarction; cardiac hypertrophy; PGF_2alpha; trauma; bone;
KW   cancer; age-related macular degeneration; wound; burn; hypertension;
KW   diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
KW   rheumatoid arthritis; Crohn's disease; amylotrophic lateral sclerosis;
KW   endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             16. .554
FT                   /*tag= a
FT                   /product= "PRO175 polypeptide"
FT   sig_peptide     16. .95
FT                   /*tag= b
FT   mat_peptide     96. .551
FT                   /*tag= c
XX
PN   WO200140464-A1.
XX
PD   07-JUN-2001.
XX
PF   11-AUG-2000; 2000WO-US022031.
XX
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   05-JAN-2000; 2000WO-US000219.
PR   24-FEB-2000; 2000WO-US005004.
PR   15-MAR-2000; 2000WO-US006884.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   30-MAY-2000; 2000WO-US014941.
PR   28-JUL-2000; 2000WO-US020710.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Godowski PJ,  Gurney AL;
PI   Hillan KJ,  Mark MR,  Marsters SA,  Paoni NF,  Pitti RM,  Wood WI;
XX
DR   WPI; 2001-381383/40.
DR   P-PSDB; AAB47287.
XX
PT   Isolated PRO polypeptide useful in treating and diagnosing a
PT   cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes
PT   mellitus, myocardial infarction, arthritis.
XX
PS   Claim 57; Fig 1; 144pp; English.
XX
CC   The sequences given in AAC85945-48 encode PRO polypeptides. PRO175 shows
CC   type II transmembrane protein typology, and portions of PRO364 show
CC   homology to members of the tumour necrosis factor (TNF) family, thereby
CC   indicating that it may be a novel member of the TNF family. PRO175 and
CC   PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a
CC   compound that inhibits PRO, diagnosing a cardio- vascular, endothelial or
CC   angiogenic disorder in a mammal by detecting PRO cDNA, treating
CC   cardiovascular, endothelial or angiogenic disorder in a mammal, and
CC   inducing cardiac hypertrophy or inhibiting endothelial cell growth or
CC   angiogenesis in a mammal. The mammal is a human which has suffered
CC   myocardial infarction, cardiac hypertrophy characterized by the presence
CC   of elevated PGF_2alpha, trauma, cancer or age-related macular
CC   degeneration. Trauma includes wounds or burns. Other treatable diseases
CC   include diabetes mellitus, osteoporosis, ischaemia, hypertension,
CC   rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
CC   endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
CC   repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC   amylotrophic lateral sclerosis, and stroke
XX
SQ   Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              1.4e-99        Length:        1964
Score:                  951.00         Matches:       177
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     4              Gaps:          0

US-09-195-368-1 (1-177) x AAC85945 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 15
AAC90563
ID   AAC90563 standard; cDNA; 1964 BP.
XX
AC   AAC90563;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO175 cDNA.
XX
KW   Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW   vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW   vulnerary; antianginal; gene therapy; cardiovascular disease;
KW   endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW   wound healing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073445-A2.
XX
PD   07-DEC-2000.
XX
PF   17-MAY-2000; 2000WO-US013705.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   30-NOV-1999;   99WO-US028313.
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PR 30-NOV-1999; 99WO-US028409.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-025251/03.
DR P-PSDB; AAB50951.
XX
PT Seventeen nucleic acids encoding PRO polypeptides which are useful in
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT disorders in a mammal.
XX
PS Claim 60; Fig 1; 182pp; English.
XX
CC The present sequence is one of seventeen nucleic acids encoding PRO
CC polypeptides. The PRO nucleic acids, polypeptides, agonists and
CC antagonists are useful for treating cardiovascular, endothelial or
CC angiogenic disorders in a mammal. Examples of these disorders include
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis
CC and lymphangitis. The PRO polypeptides and antagonists are also used to
CC prevent tumour angiogenesis and for treating periodontal diseases. They
CC are also used to stimulate wound healing and tissue regeneration. The PRO
CC nucleic acids, polypeptides and anti-PRO antibodies are useful for
CC diagnosing a cardiovascular, endothelial or angiogenic disorder
XX
SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.4e-99 | Length: | 1964 |
| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-195-368-1 (1-177) x AAC90563 (1-1964)

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Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551
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Job time : 332.795 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 18:25:49 ; Search time 277.896 Seconds
(without alignments)
2387.053 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENMPLSHSRTQGAQ.....VLKNNTYWGIILLANPQFIS 177

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=2000000000 -USER=US09195368_@CGN_1_1_409_@runat_07042004_061640_2686
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
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| 1 | 951 | 100.0 | 534 | 12 | US-10-202-062-39 | Sequence 39, Appl |
| 2 | 951 | 100.0 | 534 | 14 | US-10-272-411-9 | Sequence 9, Appli |
| 3 | 951 | 100.0 | 534 | 14 | US-10-218-547-39 | Sequence 39, Appl |
| 4 | 951 | 100.0 | 534 | 14 | US-10-272-328A-9 | Sequence 9, Appli |
| 5 | 951 | 100.0 | 534 | 14 | US-10-310-793-43 | Sequence 43, Appl |
| 6 | 951 | 100.0 | 1849 | 9 | US-09-345-790-1 | Sequence 1, Appli |
| 7 | 951 | 100.0 | 1849 | 13 | US-10-136-511-1 | Sequence 1, Appli |
| 8 | 951 | 100.0 | 1964 | 13 | US-10-080-455-2 | Sequence 2, Appli |
| 9 | 951 | 100.0 | 1964 | 13 | US-10-116-378-15 | Sequence 15, Appl |
| c 10 | 951 | 100.0 | 1964 | 13 | US-10-116-378-27 | Sequence 27, Appl |
| 11 | 281 | 29.5 | 162 | 9 | US-09-864-761-32533 | Sequence 32533, A |
| 12 | 170 | 17.9 | 397 | 9 | US-09-864-761-16032 | Sequence 16032, A |
| 13 | 107 | 11.3 | 60 | 10 | US-09-908-975-14130 | Sequence 14130, A |
| 14 | 92 | 9.7 | 50 | 15 | US-10-131-827-2732 | Sequence 2732, Ap |
| c 15 | 88 | 9.3 | 686 | 15 | US-10-027-632-287892 | Sequence 287892, |
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| c 17 | 86 | 9.0 | 755 | 15 | US-10-027-632-156281 | Sequence 156281, |
| 18 | 85.5 | 9.0 | 885 | 15 | US-10-027-632-11449 | Sequence 11449, A |
| 19 | 85.5 | 9.0 | 3441 | 15 | US-10-295-027-279 | Sequence 279, App |
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| 21 | 85.5 | 9.0 | 3650 | 15 | US-10-117-722-30 | Sequence 30, Appl |
| 22 | 84.5 | 8.9 | 1008 | 10 | US-09-951-061A-130 | Sequence 130, App |
| 23 | 84.5 | 8.9 | 1727 | 9 | US-09-834-975-942 | Sequence 942, App |
| 24 | 84.5 | 8.9 | 2829 | 15 | US-10-369-493-27503 | Sequence 27503, A |
| 25 | 82.5 | 8.7 | 1767 | 9 | US-09-822-849A-287 | Sequence 287, App |
| c 26 | 82.5 | 8.7 | 8372 | 12 | US-10-221-714A-75 | Sequence 75, Appl |
| 27 | 81 | 8.5 | 419 | 12 | US-10-085-783A-43801 | Sequence 43801, A |
| 28 | 81 | 8.5 | 419 | 15 | US-10-242-535A-43801 | Sequence 43801, A |
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| 35 | 80 | 8.4 | 3275 | 12 | US-10-205-331-15 | Sequence 15, Appl |
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| c 41 | 79.5 | 8.4 | 16086 | 9 | US-09-764-877-2385 | Sequence 2385, Ap |
| c 42 | 79.5 | 8.4 | 16086 | 15 | US-10-242-515-2385 | Sequence 2385, Ap |
| 43 | 79 | 8.3 | 611 | 15 | US-10-027-632-224303 | Sequence 224303, |
| 44 | 79 | 8.3 | 611 | 15 | US-10-027-632-224304 | Sequence 224304, |
| c 45 | 79 | 8.3 | 7505 | 10 | US-09-728-552-13 | Sequence 13, Appl |

ALIGNMENTS

RESULT 1
US-10-202-062-39
; Sequence 39, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 534
; TYPE: DNA
; ORGANISM: human
US-10-202-062-39

Alignment Scores:
Pred. No.: 3.93e-120 Length: 534
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     12            Gaps:           0

US-09-195-368-1 (1-177) x US-10-202-062-39 (1-534)

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Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
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Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
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Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 2
US-10-272-411-9
; Sequence 9, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0202
;  CURRENT APPLICATION NUMBER: US/10/272,411
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/NM_005092.1
;   DATABASE ENTRY DATE: 2002-10-07
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AF125303.1
;   DATABASE ENTRY DATE: 1999-07-02
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AF117713.1
;   DATABASE ENTRY DATE: 1999-08-09
;   RELEVANT RESIDUES: (1)..(534)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/AL031599.1
;   DATABASE ENTRY DATE: 1999-11-23
;   RELEVANT RESIDUES: (1)..(534)
US-10-272-411-9

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Query Match:            100.00%       Indels:         0
DB:                     14            Gaps:           0

US-09-195-368-1 (1-177) x US-10-272-411-9 (1-534)

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Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

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; Sequence 39, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
;  TITLE OF INVENTION:  Human Endokine Alpha
;  FILE REFERENCE: PF561
;  CURRENT APPLICATION NUMBER: US/10/218,547
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: 60/312,542
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: 60/330,761
;  PRIOR FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 534
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; TYPE: DNA
; ORGANISM: human
US-10-218-547-39

Alignment Scores:

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| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-195-368-1 (1-177) x US-10-218-547-39 (1-534)

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Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
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Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

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Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
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Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531
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RESULT 4
US-10-272-328A-9
; Sequence 9, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-9

Alignment Scores:

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|---|---|---|---|
| Pred. No.: | 3.93e-120 | Length: | 534 |
| Score: | 951.00 | Matches: | 177 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-195-368-1 (1-177) x US-10-272-328A-9 (1-534)

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Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
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Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
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Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531
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RESULT 5
US-10-310-793-43
; Sequence 43, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Disease
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07

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;  PRIOR APPLICATION NUMBER: 09/559,290
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/180,908
;  PRIOR FILING DATE: 2000-02-08
;  PRIOR APPLICATION NUMBER: 60/134,067
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/132,227
;  PRIOR FILING DATE: 1999-05-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 534
;   TYPE: DNA
;   ORGANISM: human
US-10-310-793-43

Alignment Scores:
Pred. No.:              3.93e-120       Length:         534
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     14              Gaps:           0

US-09-195-368-1 (1-177) x US-10-310-793-43 (1-534)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 180

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 240

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 300

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 360

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 420

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 480

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 531

RESULT 6
US-09-345-790-1
; Sequence 1, Application US/09345790
; Patent No. US20020099198A1
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  Human Endokine Alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/345,790
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/912,227
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0470001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1849 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..559
US-09-345-790-1

Alignment Scores:
Pred. No.:              3e-119          Length:         1849
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1 (1-177) x US-09-345-790-1 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 7
US-10-136-511-1
; Sequence 1, Application US/10136511
; Publication No. US20020168729A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A.
;  TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
;  FILE REFERENCE: 1488.0470007/EKS/PSC
;  CURRENT APPLICATION NUMBER: US/10/136,511
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 09/513,584
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: 09/345,790
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: 60/136,788
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/122,099
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: 08/912,227
;  PRIOR FILING DATE: 1997-08-15
;  PRIOR APPLICATION NUMBER: 60/024,058
;  PRIOR FILING DATE: 1996-08-16
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1849
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (53)..(559)
US-10-136-511-1

Alignment Scores:
Pred. No.:              3e-119          Length:         1849
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     13              Gaps:           0

US-09-195-368-1 (1-177) x US-10-136-511-1 (1-1849)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 88

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 148

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 208

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 268

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 328

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 388

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 448

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 508

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AATAATACCTACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 559

RESULT 8
US-10-080-455-2
; Sequence 2, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Mark, Melanie R.
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
;  FILE REFERENCE: P1150R2
;  CURRENT APPLICATION NUMBER: US/10/080,455
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: 09/195,368
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: US 60/069,661
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: US 60/065,635
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1857, 1875
;   OTHER INFORMATION: n may be any nucleotide
US-10-080-455-2

Alignment Scores:
Pred. No.:              3.31e-119       Length:         1964
Score:                  951.00          Matches:        177
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     13              Gaps:           0

US-09-195-368-1 (1-177) x US-10-080-455-2 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200
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Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 9
US-10-116-378-15
; Sequence 15, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 15
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 1857, 1875
;   OTHER INFORMATION: n may be any nucleotide
US-10-116-378-15

Alignment Scores:
Pred. No.:              3.31e-119      Length:         1964
Score:                  951.00         Matches:        177
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     13             Gaps:           0

US-09-195-368-1 (1-177) x US-10-116-378-15 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 80

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 140

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 200

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 320

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 380

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 440

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 500

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 551

RESULT 10
US-10-116-378-27/c
; Sequence 27, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 27
;   LENGTH: 1964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: 90, 108
;   OTHER INFORMATION: n may be any nucleotide
US-10-116-378-27

Alignment Scores:
Pred. No.:              3.31e-119      Length:         1964
Score:                  951.00         Matches:        177
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     13             Gaps:           0

US-09-195-368-1 (1-177) x US-10-116-378-27 (1-1964)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1944 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 1885

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 1825

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 TTCAGTTGGCTAATCTTTATTTTCTCCAATTAGAGACTGCTAAGGAGCCCTGTATGGCT 1765

Qy         61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 AAGTTTGGACCATTACCCTCAAAATGGCAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 1705

Qy         81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1704 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAGAATGGCTTATATTTAATTTATGGCCAA 1645

Qy        101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 GTGGCTCCCAATGCAAACTACAATGATGTAGCTCCTTTTGAGGTGCGGCTGTATAAAAAC 1585

Qy        121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 AAAGACATGATACAAACTCTAACAAACAAATCTAAAATCCAAAATGTAGGAGGGACTTAT 1525

Qy        141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 GAATTGCATGTTGGGGACACCATAGACTTGATATTCAACTCTGAGCATCAGGTTCTAAAA 1465

Qy        161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 AATAATACATACTGGGGTATCATTTTACTAGCAAATCCCCAATTCATCTCC 1414

RESULT 11
US-09-864-761-32533
; Sequence 32533, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32533
;   LENGTH: 162
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL031599.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;   OTHER INFORMATION: NT HIT: gi11428077, EVALUE 7.00e-83
;   OTHER INFORMATION: SWISSPROT HIT: P25003, EVALUE 1.30e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AI636075.1, EVALUE 9.60e-02
US-09-864-761-32533

Alignment Scores:
Pred. No.:              3.07e-29        Length:         162
Score:                  281.00          Matches:        52
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.55%          Indels:         0
DB:                     9               Gaps:           0

US-09-195-368-1 (1-177) x US-09-864-761-32533 (1-162)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 60

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATCATCCTGGAAGCTGTGGCTCTTTTGCTCAATAGTTATGTTGCTATTTCTTTGCTCC 120

Qy         41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlu 52
              ||||||||||||||||||||||||||||||||||||
Db        121 TTCAGTTGGCTAATCTTTATTTTTCTCCAATTAGAG 156

RESULT 12
US-09-864-761-16032
; Sequence 16032, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16032
;   LENGTH: 397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL031599.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
US-09-864-761-16032

Alignment Scores:
Pred. No.:              2.1e-13       Length:          397
Score:                  170.00        Matches:         30
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            17.88%        Indels:          0
DB:                     9             Gaps:            0

US-09-195-368-1 (1-177) x US-09-864-761-16032 (1-397)

Qy          1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGTGTTTGAGCCACTTGGAAAATATGCCTTTAAGCCATTCAAGAACTCAAGGAGCTCAG 366

Qy         21 ArgSerSerTrpLysLeuTrpLeuPheCys 30
              ||||||||||||||||||||||||||||||
Db        367 AGATCATCCTGGAAGCTGTGGCTCTTTTGC 396

RESULT 13
US-09-908-975-14130
; Sequence 14130, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/287,724
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/221,607
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14130
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-908-975-14130

Alignment Scores:
Pred. No.:              4.03e-06      Length:          60
Score:                  107.00        Matches:         20
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            11.25%        Indels:          0
DB:                     10            Gaps:            0

US-09-195-368-1 (1-177) x US-09-908-975-14130 (1-60)

Qy         72 AlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeuGluIleLeuGln 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCATCTTCTGAACCTCCTTGCGTGAATAAGGTGTCTGACTGGAAGCTGGAGATACTTCAG 60

RESULT 14
US-10-131-827-2732
; Sequence 2732, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
;  TITLE OF INVENTION:  CHRONIC INFLAMMATORY DISEASES
;  FILE REFERENCE: 506612000120
;  CURRENT APPLICATION NUMBER: US/10/131,827
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9090
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-131-827-2732

Alignment Scores:
Pred. No.:              0.000339      Length:          50
Score:                  92.00         Matches:         16
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            9.67%         Indels:          0
DB:                     15            Gaps:            0

US-09-195-368-1 (1-177) x US-10-131-827-2732 (1-50)

Qy        151 IlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGly 166
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATATTCAACTCTGAGCATCAGGTTCTAAAAAATAATACATACTGGGGT 50

RESULT 15
US-10-027-632-287892/c
; Sequence 287892, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
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;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 287892
;   LENGTH: 686
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-287892

Alignment Scores:
Pred. No.:                0.087          Length:          686
Score:                    88.00          Matches:         29
Percent Similarity:       45.26%         Conservative:    14
Best Local Similarity:    30.53%         Mismatches:      31
Query Match:              9.25%          Indels:          23
DB:                       15             Gaps:            4

US-09-195-368-1 (1-177) x US-10-027-632-287892 (1-686)

Qy          5 HisLeuGluAsnMetProLeuSerHisSerArg----------------------Thr 16
              |||||||||::::::|||          ||||||
Db        558 CATTTAGAAAGTATTCCTCGTCCCGGCAGTAGACAAAAGCCACAGGATTTATGGAAAGAG 499

Qy         17 GlnGlyAlaGlnArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeu 36
              :::|||      |||:::     :::   |||   |||||||||:::::::::|||
Db        498 GAAGGAAGGCACAGAACTGGGRCAAGGTTCTGG---TTTTGTTCTGTTATTTTGTTG--- 445

Qy         37 PheLeuCysSerPheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGlu 56
                        |||   |||:::|||:::||||||      ||||||
Db        444 --------------TCATTGTTACTGTTTGTTTTTCTTTT-TTTGAGACAGAGTCTCGC 401

Qy         57 ProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluPro 76
                 |||                   :::         |||      |||:::|||   |||
Db        400 ACTTGTCCCCCAGGCAGGAGTGCAATGGCGCACTCTTGGCTCACTGCAACCTCCA--CCT 343

Qy         77 Pro------------------CysValAsnLysValSerAspTrp 85
              |||                  |||::::::      |||  |||
Db        342 CCCAGCTTCAAGCGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGG 298


Search completed: April  8, 2004, 04:20:17
Job time : 301.896 secs
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